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LOCUS HSU19260 2359 bp mRNA PRI 04-MAY-1995
DEFINITION Human LMP1 associated protein mRNA, complete cds.
ACCESSION U19260
VERSION U19260.1 GI:675459
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2359)
Mosialos, G., Birkenbach, M., Yalamanchili, R., VanArsdale, T., Ware, C.
and Kieff, E.
The Epstein-Barr virus transforming protein LMP1 engages signalling
proteins for the tumor necrosis factor receptor family
Cell 80 (3), 389-399 (1995)
JOURNAL
MEDLINE 95163092
REFERENCE 2 (bases 1 to 2359)
AUTHORS Mosialos, G.
TITLE Direct Submission
SUBMITTED (29-DEC-1994) George Mosialos, Microbiology and Molecular
Genetics, Harvard Medical School, 75 Francis Street, Boston, MA
02115, USA
FEATURES
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QY	2228	acatgatttttcttcccttaacttgaaccccaaaaacacacacacacacacagtgg	2287
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LOCUS	HDNCAP1A	2240 bp	PR1 12-JUN-1995
DEFINITION	Homo sapiens CD40-associated protein (CAP-1) mRNA, complete cds.		
ACCESSION	L38509		
VERSION	L38509.1	GI:695357	
KEYWORDS	CD40-associated protein.		
SOURCE	Homo sapiens fetus brain CDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Sato,T., Irie,S. and Reed,J.C.		
TITLE	A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40		
JOURNAL	FEBS Lett. 358 (2), 113-118 (1995)		
MEDLINE	95129692		
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BASE COUNT	637 a 509 c 604 g 490 t		
ORIGIN			
Query Match	Best Local Similarity	96.3%	Score 2062.6; DB 10; Length 2240;
Matches 2185; Conservative	0; Mismatches	4; Indels	80; Gaps

OY	76	agaagtgaatgcacattggttaaggtcccaagacgaagtcagaatcagaactagatccagaa	135
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OY	136	acctgagccctcgagctccct-gctccctcactcttctaagatcagctgtccctgaaagaaga	194
Db	61	ACCTGCGCTCCGCGCTCCTGGCTCCCTTCTTCTTAAGATCGCTGTGTCGACAGAAAGAA	120
OY	195	actccctcttctaanaatgagtgctcgagtaaaaaagatgagactccctcgcgctcgagac	254
Db	121	ACTGCTCTTCTCTTAATGAGAGTGGAGTATAAAAGATGAGATCTCCCTGCGGCGCTGAGAC	180
OY	235	taaccgcgcgtctaaagctgcacatgcgcgcagtgctgaggacgcagcttctgtccctga	314
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OY	315	acaaggaagtgtacaaaggaanaagttgtgaaagacgctggaagaaagataaagtgtgaga	374
Db	241	ACAAAGAGCTTACAAAGGAAAGTTGTGAAAGACCGTGaagAACAAATCAAACTGTGAGAA	300
OY	375	gtgcacacctggtgctgtgcagccccgaagcagacgcagtgtygagcacgccttctgagag	434
Db	301	GTGCGACCTGGTGGCTGTGAGCCCGAAGCAGACCGAGTGTGGGCAACGGTTCTGGAGAG	360
OY	435	ctgcaatgagcgccctgctgagctctccaagtccaaaatgacagcgtgtcacaagagacat	494
Db	361	CTGCAATGCGCGCCCTCGCTGAGCTTCTTAATCCAAATGTACAGCTGTCAAGAGAGCAT	420
OY	495	cgtaagaataagtggtttaagtaattctcacaagaggaattctgacctcagat	554
Db	421	CGTTAAAGATAGGTGTTTAAAGGTAATTCCTCCAAAGAGAAATTCGTGCTTCAGAT	480
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Db	481	CTATTGTGCGAATAAAGCAGAGGTTGTGAGAGCATTAACCGTGGAGACATCTGCTGCT	540
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Db	721	CGAGTGTCCCTGCGTGGTGGTGTCTCTCCCTCAAGTGGAGGCTCCAGACATCTCCTGAG	780
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Db	781	GAGCG-----	785
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OY	1032	cttgtgtgagaataaaggtgtgagaaaaaacaagagcatcaaaagtttgcacatccagat	1091
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OY	1092	atgtagctttgaaatgaaattgagagacaagaagaaatgcttcgaaataatgaaatccaa	1151
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Db	2146	AGCTGGACATGTACCATGTTTAAAGTAAAAGAAGATTATGAATAAGTA	2194
RESULT	5		
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DEFINITION	Mus musculus TRAF-related protein (TRAFam) mRNA, complete cds.		
ACCESSION	U33840		
VERSION	U33840.1	GI:1488197	
KEYWORDS			
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Wang, X., Bornslaeger, E.A., Haub, O., Tomihara-Newberger, C., Lonberg, N., Dinulos, M.B., Distèche, C.M., Copeland, N., Gilbert, D.J., Jenkins, N.A. and Lacey, E.		
TITLE	A candidate gene for the amnionless gastrulation stage mouse mutation encodes a TRAF-related protein		
JOURNAL	Dev. Biol. 177 (1), 274-290 (1996)		
MEDLINE	96299439		
REFERENCE	2 (bases 1 to 7331)		
AUTHORS	Wang, X.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-AUG-1995) Xin Wang, Molecular Biology, Memorial Sloan-Kettering Cancer Center, 1275 York Avenue, New York, NY 10021, USA		
FEATURES			
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misc_feature	774..959 /gene="TRAFam" /note="encodes zinc ring domain"		
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Db	676	CACITCCACCTTAACCCACCCCTTAAGCTGCAAGCTGATGCGGGCCAGG--GTCCTGTC	732		
Qy	305	ttgtccctgaacaagaagagtttaacaagaagaatttggttaagaacgcttgtagagcaagtaca	364		
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Qy	365	agtgagagaagtgtcacactgt	424		
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Qy	485	aagagaagatcgtttaagaataagtggtttaagaataattgtgtgtgtgtgtgtgtgtgtgtgt	544		
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Qy	722	accggtgaagccacatgtacagccacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	781		
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Qy	782	acgaagaagacccagctgt	841		
Db	1213	ATGAAGACACAGATTTGCTCCTGT	1272		
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Qy	902	gtgaatttaagtgatgt	961		
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Qy	1022	agaagaatttcctgt	1081		
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Qy	1082	acaatcagatcgt	1141		
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ACCESSION      AL117209
VERSION        AL117209.2  GI:6981780
KEYWORDS       HTG; HTGS_PBASE2; HTGS_DRAFT.
SOURCE         human.
ORGANISM       Homo sapiens
REFERENCE      Mammalia: Eutheria; Primates; Carnivora; Homnidae; Homo.
TITLE         1 (bases 1 to 161000)
JOURNAL
COMMENT        Genoscope.
                Direct Submission
                Submitted (14-OCT-1999) Genoscope - Centre National de Sequencage :
                BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
                On Feb 16, 2000 this sequence version replaced gi:6065792.
                IMPORTANT: This sequence is unfinished and does not necessarily
                represent the correct sequence. Work on the sequence is in progress
                and the release of this data is based on the understanding that the
                sequence may change as work continue. The sequence may be
                contaminated with foreign sequence from E.coli, yeast, vector,
                phage, etc.
                Contig order : 4 6 5, 1000 N's separate segments
                Contig 4 : length 23278 bp
                Contig 6 : length 117351 bp
                Contig 5 : length 27145 bp
                * NOTE: This is a 'working draft' sequence. It currently
                * consists of 3 contigs. Gaps between the contigs
                * are represented as runs of N. The order of the pieces
                * is believed to be correct as given. However the sizes
                * of the gaps between them are based on estimates that have
                * provided by the submittor.
                * This sequence will be replaced
                * by the finished sequence as soon as it is available and
                * the accession number will be preserved.
                * 1 18859: contig of 18959 bp in length
                * 18960 19959: gap of 1000 bp
                * 19960 137310: contig of 117351 bp in length
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                Best Local Similarity 99.8%; Pred. No. 4.1e-210;
                Matches 998; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	123577	gcctacgcgacatgacctgcgcttccaggtccttgcgacgcgcacactpaaatgagatgc	123636
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QY	1520	tgctcccttaagcagcccttctacactggttacttggctatlaagatgtygtccagg	1579
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Db	123937	gcacagacttcacaagaagcccactgtygaagaatgaataatcgcctctgtctgcacagcttgg	123996
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Db	124117	cagaagcgaactcctctggyggatattgaaccggtctgcttcaactgaagctctgcgctc	124176
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Db	124177	agaaaaggaaccttctgagcagaggaagcggcagaagcggagcgttgcggcgaggaga	124236
QY	2060	gcacagcgagagcagcactgtaacagtttataatagactgacacactcaactcgtga	2119
Db	124237	gcacagcggtgagcagcactgtaacagtttataatagactgacacactcaactcgtga	124296
QY	2120	attattatccttcaacaagaataatattgctgtcagagaagtttcatattcatlttt	2179
Db	124297	attattatccttcaacaagaataatattgctgtcagagaagtttcatattcatlttt	124356
QY	2180	aagagtcagtaattagatgtyggaacaatataatgctcaaaagaagaatgatltttc	2239
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QY	2240	tttccttaacttgaaccccaaaaaaacacacacacacacacagcttgggatagctgaca	2299
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QY	2300	tgctcagcatgttaagtaaaagagaattatgaaataga	2339
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RESULT	8		
LOCUS	AF110908	5844 bp	09-MAY-1999
DEFINITION	Homo sapiens TNF-receptor associated factor-3 (TRAF-3) mRNA, partial cds; and 3' UTR.		
ACCESSION	AF110908		
VERSION	AF110908.1	GI:4761209	
KEYWORDS			

[illegible]

Oy	2233	atttcttcctaactttgaacaccacaacacacacacacacacacgtyggagtag						2293
Dd	421	ATTTTCTTCCTTAACACTTGAAACCACAAAAAACACACACACACACACAGCGGGGATAG						480
Oy	2293	cttgacatgtcagaatgttaagataaaaggagaattatgatagta						2339
Dd	481	CTGCACATGTCCAGCATGCTTAGTAAAAGAAGAAATTATGAATAAGTA						527
RESULT	9							
LOCUS	G15867	425 bp	DNA	STS	19-JAN-1996			
DEFINITION	human STS CHLC.UTR_05642_U15637.P65624 clone UTR_05642.U15637.							
ACCESSION	G15867							
TITLE	G15867.1 GI:1161756							
KEYWORDS	STS sequence; primer; sequence tagged site;							
SOURCE	human vector-pCPI host-E.coli dut+ung+ (DH10B) Marker Selected genome DNA prepared from xy individual of French nationality.							
ORGANISM	Homo sapiens							
	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;							
	Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Channath-							
	retropoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Prima-							
	Cetartihini; Hominoidea; Homo.							
REFERENCE	I (pass 1 to 42)							
AUTHORS	Murray,J., Sheffield,D.V., Weber,J.L., Duyk,G. and Buelow,K.H.							
JOURNAL	Cooperative Human Linkage Center Unpublished (1995)							
COMMENT	Synonyms: UTR_05642,U15637, CHLC.UTR_05642,U15637.T36426 Contact: Dr. Jeffrey C. Murray Noif Department of Pediatrics, Iowa City, IA 52242, USA Tel.: (319) 356-3508 Fax: (319) 356-3347 Email: jeff-murray@uiowa.edu							
	Primer A: AGAGCACACCTGCACACGTT Primer B: CTGCATGTCCAGCTATCCC STS size: 238 PCR Profile:							
	denature: 30 seconds at 94 degrees C annealing: 75 seconds at 55 degrees C extension: 15 seconds at 72 degrees C PCR cycles: 27 extension: 6 minutes at 72 degrees C Template: 30ng genomic DNA Primer: each 1.5 pmole dNTPs: each 200 uM Taq Polymerase: 0.3 units Total Vol: 10 ul							
	Protocol:							
	Buffer:							
	MgCl2: 1.5mM KCl: 50mM Tris: 10mM pH: 8.3							
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OY	506	aggctgttaaggaataatgctgcacagaaganaattcgtgccttcacagatactgttcgga	565
Db	218	AGGTTTAAAGACAAATGTGTGCAAAAAGAGAGTCCTCAACTATATGTATTTTGAGAGA	277
OY	566	atgaaagcagaggtgtgtgcagagcagttaatgctgggacatcgtgtgcatttaaaaaatg	625
Db	278	ATGCTCTCGATGTGTAATGTC-----CAAGGTTATTTCTGGGCCGCTACCGAGATCACTTACAC	334
OY	626	attgcacattggaagaacttcacatgctgtgcctgcctgcacaaagaagaagctgtgaga	685
Db	335	AGTGGTTATTTCACACCTGTGAGTGCTTCTAATGAGAAGTCCCGGAGCCAGTCTTAACGA	394
OY	686	aagacctgcagaccacgctgtgagaagcgctgtataataccgggaagacacatgcaaccact	745
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OY	746	gcaagatgcaggttccgatgatcgcgctgtaagaaacacgaagacacgagcttccctcg	805
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OY	806	tgtgtgttccctgcctccacaaagtgacgcttccagacttccgtgagagcaggtttgagtg	865
Db	515	AACCCGATATTTGTGCCAACACT--GTGCGAGATTAATTCTTAAAACTGAGGATGATG	571
OY	866	cacactgtcagagtgctgctcaatgccccacacgtgtagttttaagcgctatgctgcg	925
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Db	812	AGGAGTTCAACCACTTTGCACAGTTGTTTGGCAAAATGGAAACTTCTCCCAACATCC	871
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Db	872	AG-----GTTTGTGCCAGTCCACTTGACACAGTCCACTTGCTAGAGCTCAAGTCACTCAAT	928
OY	1226	tcgcgcgaagaactgtgaggaagcagacagcatalgaagacagcgctgtgagtcctccagaacc	1285
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RESULT 15
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VERSION
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AC053507 49960 bp DNA HTG 16-APR-2000
Homo sapiens clone RP11-318L16, LOW-PASS SEQUENCE SAMPLING.
AC053507.1 GI:7577633
HTG: HTGS_PHASE0.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 49960)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 49960)
Waterston, R.H.
Direct Submission
Submitted (16-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
Center project name: H_NH0318L16.
* NOTE: This record contains 94 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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12287: contig of 803 bp in length
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12815: contig of 518 bp in length
12825: gap of unknown length
13342: contig of 517 bp in length
13352: gap of unknown length
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19647: contig of 516 bp in length
19648: gap of unknown length
20176: contig of 519 bp in length
20186: gap of unknown length
20703: contig of 517 bp in length
20713: gap of unknown length
21230: contig of 517 bp in length
21240: gap of unknown length
21241: contig of 517 bp in length
21757: gap of unknown length
21767: gap of unknown length
22284: contig of 517 bp in length
22294: gap of unknown length
22811: contig of 517 bp in length
22821: gap of unknown length
23338: contig of 517 bp in length
23348: gap of unknown length
23865: contig of 518 bp in length
23876: gap of unknown length
24380: contig of 504 bp in length
24387: gap of unknown length
24391: gap of unknown length
24907: contig of 517 bp in length
24917: gap of unknown length
25436: contig of 519 bp in length
25446: gap of unknown length
25964: contig of 518 bp in length
25965: gap of unknown length
26341: contig of 367 bp in length
26342: gap of unknown length
26866: contig of 515 bp in length
26867: gap of unknown length
27380: contig of 504 bp in length
27390: gap of unknown length
27908: contig of 518 bp in length

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QY	610	gtgacattaaanaaatgatctgcatctttaagaactccatgtgctgctcgaattgcaaa	665
Db	454	GTGCATTTAAAAAAGATGGCCATTTTGAANAACCTTCATGTGTGCGTCTGACTGCAAA	3955
QY	670	gaaaaagctcttgaggaagaagccctgcgagaccagctlgagaaagcgtgtlaataccggyg - a	728
Db	394	GAAAAGGCTCTTGAGGAAAAGACCTGGGAGNCCACGCTGGAGAGGCGGTAAATTCCGGGAA	3353
QY	729	agccacatgcagagccacctcaagaatcagaattccgaatatacgcgctgtgaagaaacgagaa	788
Db	334	AGCCACATGCAAGCCACTCCHAAAGTCAAGTTCGAGTGTCCGGTGGCGAAGAACGAGAA	2757
QY	789	caaccagctgccctcgtcgtgtgtgtgtccctgcacctacaagtgtcagagcgtlccagactccct	848
Db	274	CACGACGTCCCTCGTGGTGTGTGTCTCTGCGCTACAAATGTGACGCGTCCAGACTCTCT	215
QY	849	gagagaagcagtttgatgtcacacactgtcagagttgtgtcaatgccccagcaacctgtagttc	908
QY	214	GAGGAGCCAGTGTGAATGCACACTGTGTCAAGATGTGTCAATGCCCCGACACCTGTACTTT	155
QY	909	taagagcagatgctgctgctttctcaaggggacaacacagcagaatcaaggcccaacgagagcag	968
Db	154	TAAAGGCTATGGCTGTGCTTTTTCAGGGGACAAAACAGCAGATTCAAAGCCACAGAGGCCAC	95
QY	969	ctccgcgctgcagacacgtcaaacctgtctgaagagtgtagcaactcgtctgaaagaaggt	1027
Db	94	GTCGCCGCTGCACAACGCTCAACCTGTCTGAAGATGTGAGCAACTCCGACGAAAAAAGGT	35
QY	1029	tttcctgtgtgcagaatgnaatgtcagaaaaaaa 1061	
Db	34	TTTCCTGTGTACGAAGAAGTGTGAAAAAAA 2	

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RESULT 2
LOCUS AI344113/c
DEFINITION AI344113 568 bp mRNA EST 08-APR-1999
            tc22b03.x.1 NCI_CGAP_Col16 Homo sapiens CDNA clone IMAGE:2062637 3
            similar to TR:Q13947 Q13947 CD40-ASSOCIATED PROTEIN. ; mRNA
            sequence.
ACCESSION AI344113
VERSION AI344113
KEYWORDS AI344113.1 GI:4081319
SOURCE EST.
ORGANISM human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 568)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck,
            M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Cent
            clone distribution: NCI_CGAP clone distribution information can
            found through the I.M.A.G.E. Consortium/ILMIL at:
            www-bio.linnl.gov/dbirp/image/image.html
            Insert Length: 651 Std Error: 0.00
            Seq primer: -40up from Glbco
            High quality sequence stop: 448.
FEATURES
            Location/Qualifiers
                1..568

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FEATURESOURCE
Location/Qualifiers
1. 568
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone IMAGE:2062637"
/clone_id="NCI_GGAP_Col6"
/tissue_type="colon tumor; RER+
/ab_host="DH108"
```

/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Plasmid DNA from the normalized library NCI.CGP.Colo was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clonoids 1057416-1061255, and 1144584-1145351).
 Subtraction by Bento Soares and M. Fatima Bonaldo. "

	Query March Best Local Similarity Matches	24.2%; 99.8%; 567;	Score 566.4; P:ed. -0.48e-139; Conservative	DB 38; Length 568; Indels 0;
QY	1771	aagaagccacatgagagatgaaatcgcctctgctcgcccaagctcttctgtgcccgaact	1830	
Db	568	AAGAAGCCCACTGGAAGATGAAATATCGCCTTGCTGGCTGCCAGTCTTGTCGCCCAACT	509	
QY	1831	gtctagaatgaggcatatataaagttgtaaatcttttataaagtcatactgtagt	1890	
Db	508	GTCTAAGAAATGGGACATATATTAAGATGATACAAATTTTATTAAGATATGTGGAT	449	
QY	1891	acttcgcatctgcgcgcatccctataagtagcttgaggagtgtagatttagcagaagcaac	1950	
Db	448	ACTTCGGATCTGCCCATCCCTCATTAAGTAGTCGGGAGAGTGTGATTTAGCAAGAGCAAC	389	
QY	1951	tcctctggygatttgaaaccgctctgctcttcacatgagtcctcgcgctcagaagaagacc	2010	
Db	388	TCCCTCTGGGGGATTTTAACCGGCTCTTCTTCACTAGGCTCCGCGCTCAGAAAGGACC	329	
QY	2011	tttggaagacggaagagcgacagaagcggaagcgctgcccgcgaggaagccacgcgaga	2070	
Db	328	TTTGGAACACGGAAGAGCGGCAAGGCGGAGCGCTGCGGGGGAGGAGGACGCGTGA	269	
QY	2071	gcaacacatgcacgctttcataatagacatgcacacactcgaactctgaaagatctatctac	2130	
Db	268	GCAACACTGACAGGTTTTTAATATAGACTAGCCACACTTACACTGTAAGAAATATTTATTC	209	
QY	2131	ttcaacaagaataatattgctctgcagaagaagtttcatatttcatattttaaagctagt	2190	
Db	208	TTTCAACAGATTAATATATGTGCTGCACAGAGAGGTTTTTCATTTTCAATTTTAAAGATCTAGT	149	
QY	2191	taattaagctgggaacaacataatgctctcaacaagaagaacatgattttcttccttaact	2250	
Db	148	TAAATTAAGGTGGAAAACATATATGCTTAACCAAAAGAAACATGATTTTCTTCCTTAAACT	89	
QY	2251	tgaacacccaataaaacacacacacacacacacgcttggygatactgtagactgttcagcagt	2310	
Db	88	TGAACACCAAAAAAACACACACACACACACAGCTGGGATAGCTGACATGTCAATGT	29	
QY	2311	taagtaaaaggaatattatgaatactgt	2338	
Db	28	TAACTAAAGGAGAAATTTAAGAAATGT	1	

RESULT	3			
LOCUS	AL135246			
DEFINITION	AL135246	587 bp	mRNA	EST
ACCESSION	DKFZP162M1613	-1762	(synonym: hmel2)	Homo sapiens cDNA clone
VERSION	AL135246			
KEYWORDS	AL135246.1	GI:6603433		
SOURCE	EST.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Emkaryovts; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 587)			
	Ansoerge,W., Wilkner,U., Mewes,W., Well,B. and Wiemann,S.			
	EST (Ansoerge,W., Wilkner,U., Mewes,H.W., Well,B. and Wiemann,S.)			

JOURNAL Unpublished (1999)
On Apr 7, 1998 this sequence version replaced g1:3035257.
COMMENT Contact: Ansgore W

MPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Cloned from S. Mleemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ). Email: s.mleemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZ/62M1613) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcentum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

FEATURES
source 1..587

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZ/62M1613"
/clone_id="762 (synonym: hmel2)"
/tissue_type="melanoma (Mewo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 176 a 129 c 139 g 143 t
ORIGIN

Query Match 24.0%; Score 560.8; DB 47; Length 587;
Best Local Similarity 99.2%; Pred. No. 1.5e-137;
Matches 585; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

OY 1698 gctgattgacgagggctcctcgcacgtcatttggagatgattcaccgaccgacaa 1757
DB 1 GGTATGATGATGAGGGGCTCTCGACGTCATTTGGAGATGATCAAGCCGACCCCA 60
OY 1758 cagcagcagcttcaagaagccacgagagatgatatccgctctggtgccagctct 1817
DB 61 CAGCAGCAGCTTCAAGAGCCCGAGAGATGATATCGCTCTGGTGGCCAGTCTT 120
OY 1818 tctggcccaaacgtctctagaagaatgagacatattaaagatgatacatttattaa 1877
DB 121 TGTGGCCCAAACTGTTCTAGAAATGGGACATATTAAGATGATACATTTTATTAA 180
OY 1878 agtcatagtgatctcctggatcgcgcgacatccctgataagtagctgggaggtgattt 1937
DB 181 AGTCATAGTGATCTCGATCTGCCGATCCCTGATAGTAGCTGGGAGAGTGGATT 240
OY 1938 agcagaagcaactcctcgtgggagatttgaaccggtctgtctcactgaggtcccgcc 1997
DB 241 AGCAGAAGCAACTCCTCTGGGGGATTGACCGGCTCTCTCACTAGAGTCTGGCCG 300
OY 1998 tcagaagaagcacttctgagacgaggaagcgacgaagcgagcgctgcccggcgag 2057
DB 301 TCAGAAAAGGACCTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
OY 2058 gagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2117
DB 361 GAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
OY 2118 gaattattatccttcaagaagataatattgctcgaagaagaggtttcatttcaatt 2177
DB 421 GAATTAATTAATCTTCAAGAAAGTAATATTGCTGTCAGAGAGGTTTTCATTTTCA 480
OY 2178 ttaaaagatcttaataagtgagaaacataatgctctaaacaaagaacatgattt 2237
DB 481 TTAAGATCTTAATTAAGTGGAAACATATATGCTAAACAAAGAAACATGATTTT 540
OY 2238 tcttcccttaacttgaaacacacacacacacacacacacacacacacacacacac 2287
DB 541 --CTCCTTAACCTGAAACAC--AAAAACACACACACACACACACACACACACAC 587

RESULT 4

LOCUS A1582315/c

DEFINITION A1582315 661 bp mRNA EST 14-DEC-1999

ACCESSION t96606.x1 NCI-CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2213771 3'

VERSION similar to TR:Q13947 Q13947 CD40-ASSOCIATED PROTEIN.; mRNA

KEYWORDS A1582315

SOURCE EST.

ORGANISM human.

REFERENCE Homo sapiens

AUTHORS Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

On Oct 30, 1998 this sequence version replaced g1:3814596.

Contact: Robert Strausberg, Ph.D.

Tel.: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/brp/image/image.html

Insert length: 719 Std Error: 0.00

Seq primer: -40UP from Glibco

High quality sequence stop: 426

POLYA-NO.

FEATURES
source 1..661

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2213771"

/clone_id="NCI-CGAP_Lu19"

/tissue_type="squamous cell carcinoma, poorly

differentiated (4 pooled tumors, including primary and

metastatic)"

/dev_stage="adult"

/lab_host="DH10B (phage-resistant)"

/note="Organ: Lung; Vector: pT730-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from

pooled lung tumor tissue, and was then primed with a Not I

- oligo(dT) primer. Double-stranded cDNA was ligated to

Eco RI adaptors (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of the modified

pT73 vector. Library went through one round of

normalization. Library constructed by Bento Soares and M.

Fatima Bonaldo.

BASE COUNT 164 a 147 c 131 g 219 t

ORIGIN

Query Match 22.0%; Score 513.8; DB 41; Length 661;
Best Local Similarity 97.4%; Pred. No. 4.1e-125;
Matches 554; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

OY 1771 aagaagccacctggaggaatgatatgcctctgctgctcccaagctcttgggccaact 1830
DB 661 AAGAGCCACCTGGAGGAGATGAAT-TCGCTCTGCTGCCAGTCTTGTGGCCCAACT 603
OY 1831 gttcagaagaatggagacataattaaagatgatacaattttatataagtcataagat 1890
DB 602 GTCTTAGAAGATGGGACATATATTAAAGATGAT-CCATTTTATTAAAGTCAATAGAT 544
OY 1891 acttgagatctgcccagatccctgataagtagctgggaggtgagatttagcagaagcaac 1950

QY 475 acagcgtgtcgaagagcagcgtttaaagataaggtgtttaaagataatgtctgcagaaga 534
 DB 312 ACAGGCTGTCAAGAGAGCATGCTTAAGATAGGTTTAAGGATATGCTGCAGAGA 253
 QY 535 gaattctgtgtcttcacatctatgtcgaatgaagcagaaggtgtgcagaagcagta 594
 DB 252 GAAATTCGGCTCTTCAATCATATGTCGGAATGAAGAGAGGTTGTGCAGACGAGTTA 193
 QY 595 atgcctggagacat---ctgtgtcatttaaaatgtccattttgaagaattccatgt 651
 DB 192 ACCTGGGACATCTCTGTCGATTTAAATAATGATGCTATTGAAAGACTTCATGT 133
 QY 652 gtgcgtcttcagcagcagaagaaggtcttcgaagaagacctgcagaccagctggagaag 711
 DB 132 GTGCTCTGACATGCAAGAAAGAGCTTTGAGGAAAGACCTCGAGACACTGGAGAAG 73
 QY 712 ggcgttaataacccgggaagccacatgcagccactgcagaagagtcaggttcgatgcgcg 771
 DB 72 GCGTGAATATACCGGGAAGCCACATGCAGCCACTGCAAGAGTCAAGTTCGATGATCG-G 14
 QY 772 ctgcagaacacg 784
 DB 13 CTACAGAAACAG 1
 RESULT 8
 AA194061/c 658 bp mRNA EST 14-FEB-1997
 LOCUS z137d03.r1 Soares_NHMPu.S1 Homo sapiens cDNA clone IMAGE:65573 5'
 DEFINITION similar to TR:G695358 G695358 CD40-ASSOCIATED PROTEIN. ;, mRNA
 sequence.
 ACCESSION AA194061
 VERSION AA194061.1 GI:1783807
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 658)
 AUTHORS Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevaakis, E., Waterston, R., Williamson, A., Woldmann, P. and
 Wilson, R.
 TITLE The WashU Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 High quality sequence stop: 327.
 FEATURES
 Source
 1. 658
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="GDB:5427605"
 /db_xref="taxon:9606"
 /clone="IMAGE:65573"
 /clone_lib="Soares_NHMPu.S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: p7T73D-Pac
 (Pharmacia) with a modified polylinker; Site: 1: Not 1;
 Site 2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBH, pregnant uterus
 NBHPU, and fetal heart NBH19W) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA

BASE COUNT 143 a 173 c 155 g 176 t 11 others
 ORIGIN
 Query Match 19.1% Score 446; DB 22; Length 658;
 Best Local Similarity 91.6%; Pred. No. 3.5e-107;
 Matches 589; Conservative 0; Mismatches 39; Indels 15; Gaps 11.
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."
 QY 154 gtccctaccccttcgaagatgcgtcttcgacaaagaagaccccttcctcaaatg 213
 DB 647 GCTCCCTACTCTCTCAAGA NGCTTNTGACAGAAAGAACCTTTCTCCNTAATG 589
 QY 214 gattcgaagtaaaagatgacac-tcctggcgcgctgcagactaa-cccgcgcgtaaagc 271
 DB 588 GAGTCGAGTAAAGATGAGACTCTTCTGCGCNGCTTCAGACTAACCCGCCCTAAAGC 529
 QY 272 tgcacactgaccg-cagtgcctggagcccaagttttgtccctgaacaagaggttaacag 330
 DB 528 TNCACACTGACCCNCCAGTGTGAGACCCCAAGTNTGTCCTGAAACAAGAGATTACAG 469
 QY 331 gaaagattgtg-aagaccgttggagagac--aagtaaaagtgtgaaagtgc--accctg 385
 DB 468 GAAAGATTGTGAAAGACCGCTGGAGACCAAGTACCAAGTGTGAAATGCCCACTTGG 409
 QY 386 tgcgttg-cagcccgcaagcagacagctgtggc-accgctctgc-gagagctcatg 442
 DB 408 TGCTGTGCCAGCCGGAACAGACAGCGAGTGTGGCAACCGCTTCTCGGAGAGCTCATAG 349
 QY 443 cggccctgcagctcttcaagtcacaaatgtaacgctgtcaagaagcagcgtttaaag 502
 DB 348 CGGCCCTGCTGAGCTCTTCAAGTCCAAATGATACAGCTGTCAAGAGACATCGTTAAG 289
 QY 503 ataaagtgttaagatatgtctgcagaagagaatctgtcttcaagatctcttgc 562
 DB 288 ATAAAGTGTTAAGATATGCTGCAAGAGAAATATGCTCTTCAAGATCTATTTGTC 229
 QY 533 ggaatgaagaagaaggtgtgtcagaagcagttaatgtctggacat--ctgtgcattaa 619
 DB 228 GGAATGAAGACAGAGGTTGTGCAAGAGATTAAAGCTTGACATGTGCTGGCATTTAA 169
 QY 620 aaaaatgattccatttgaagaacttccatgtgtgtcgtcgtcagcagaagaagagctct 679
 DB 168 AAATGATTGCCATTTTGAAGAACTTCCATGTGCTGCTGCAAGAAAGAGTCT 109
 QY 680 tgaagaagacctgcagacacacgtgtggaagagcgctgtaaatccgggaagccaatgca 739
 DB 108 TGAGGAAAGACCTCGGAGACCAACGCGGAGAGGCTGTGAATACCGGGAAGCCACATGCA 49
 QY 740 gccactgaagatcaggttcagatgcgcgcgtcagaaca 782
 DB 48 GCCACTGCAAGAGTCAAGTTCGATGANTCCGCTGCAGAAACA 6
 RESULT 9
 AW589978/c 404 bp mRNA EST 22-MAR-2000
 LOCUS hg28b12.x1 NCI-CGAP-G6 Homo sapiens cDNA clone IMAGE:2946911 3'
 DEFINITION similar to TR:Q13947 Q13947 CD40-ASSOCIATED PROTEIN. ;, mRNA
 sequence.
 ACCESSION AW589978
 VERSION AW589978.1 GI:7277103
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 404)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Db 375 CCCTGAACAGAGGTTACAGAGAAAAGTTTGAAGACCGTGAGACAGTACAGATG 434

Qy 369 tgaagaatgccacc-tggtgctgtcagccgaagcaga-ccgaatgtgagca-ccgctt 425

Db 435 TTAGAGAGTCCACCTTGGTCTGTGTGACGCCGAGACGACCGAGTGTGGACCCGCTT 494

Qy 426 ctgcgagagatgcatg 441

Db 495 CTGCGAGACCGCTGATG 510

RESULT 11

LOCUS A1393367 477 bp mRNA EST 30-MAR-1999

DEFINITION tga4e06.x1 Soares NFL.T.GBC.S1 Homo sapiens cDNA clone

IMAGE:2111650.3' similar to TR:Q13947 Q13947 CD40-ASSOCIATED

PROTEIN: ; mRNA sequence.

ACCESSION A1393367 GI:4222914

VERSION A1393367

WORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 477)

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

TELE: (301) 496-1550

EMAIL: Robert.Strausberg@nih.gov

THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LNL; CONTACT THE IMAGE CONSORTIUM (info@image.lnl.gov) FOR FURTHER INFORMATION.

INSERT LENGTH: 1222 Std Error: 0.00

SEQ PRIMER: -40UP from G1bco

HIGH QUALITY SEQUENCE STOP: 322.

FEATURES

source

1. 477

Location/Qualifiers

1. 477

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2111650"

/clone_1lb="Soares_NFL.T_GBC.S1"

/lab_host="DH10B"

/note="organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 113 a 143 c 143 g 78 t

ORIGIN

Query Match 15.4%; Score 359.6; DB 39; Length 477;

Best Local Similarity 95.0%; Pred No. 2.2e-84;

Matches 382; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

Qy 10 acgagccgagccgcccctgtgagccgagccgagcagccgagatgaggaatgag 69

Db 75 AGCGCGCGCGCGCCCTGTGAGCGCGCGAGGAGGAGCGGAGATGAGAAATGAG 134

Qy 70 gcccaagaagtgtatgcacattgttaaggtccagagagagtcagaatcagaactaga 129

Db 135 GCCCAAGAAGTGTATGCCACTTGTGTTAAGTCCAGAGCAGGTCAAGATCAGACCTAGGA 194

Qy 130 tcaagaactgtctctgtctct-gctccctactcttctaagagatcgctgtctctgacag 188

Db 195 TCAGAAACCTGGCTCCTGTGCTCTGCTCCCTACTCTTCTTAAGATCCGCTGCTGACAG 254

Qy 189 aagaagaacccctcttctctaaatgtgagtcgataaagaatgagctctccggcgct 248

Db 255 AAGAGAACTCCCTCTTCCCTAAATGAGTGAATAAAGAGGAGCTCCCTGGCGCGCT 314

Qy 249 gcaactaaccccgccgctaaagctgacactgaccgcaagtgtctggagccagtttgt 308

Db 315 GCAGACTAACCCCGCGCTTAACCTGACACTGACCCGCACTGCTGGACCCCGTTTGT 374

Qy 309 cccctgaacagagaggttacaaggaagtttgtgaagaccgtgaggaagataagtg 368

Db 375 CCCTGAACAGAGGTTACAGAGAAAAGTTTGAAGACCGCTGAGACAGTACAGATG 434

Qy 369 tgaagaatgccacc-tggtgctgtcagccgaagcaga-ccgaatgtgagca-ccgctt 425

Db 435 TTAGAGAGTCCACCTTGGTCTGTGTGACGCCGAGACGACCGAGTGTGGACCCGCTT 494

RESULT 12

LOCUS N76469/c 475 bp mRNA EST 02-APR-1996

DEFINITION yz87d10.r1 Soares multiple_sclerosis_2NDHMP Homo sapiens cDNA clone IMAGE:290035.5' similar to PIR:A55649 A55649 TNFR-associated protein LAPI - human ; mRNA sequence.

ACCESSION N76469

VERSION N76469

WORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 475)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,T., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.

THE WASHU-MERCK EST PROJECT

UNPUBLISHED (1995)

ON JAN 6, 2000 THIS SEQUENCE VERSION REPLACED GI:6676353.

CONTACT: Wilson RK

WASHINGTON UNIVERSITY SCHOOL OF MEDICINE

4444 FOREST PARK PARKWAY, BOX 8501, ST. LOUIS, MO 63108

TEL: 314 286 1800

FAX: 314 286 1810

EMAIL: est@wustl.edu

THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LNL; CONTACT THE IMAGE CONSORTIUM (info@image.lnl.gov) FOR FURTHER INFORMATION.

SEQ PRIMER: reverse ET

HIGH QUALITY SEQUENCE STOP: 291.

FEATURES

source

1. 475

Location/Qualifiers

1. 475

/organism="Homo sapiens"

/db_xref="GDB:3905875"

/db_xref="taxon:9606"

/clone="IMAGE:290035"

/clone_1lb="Soares_multiple_sclerosis_2NDHMP"

/sex="male"

/tissue="multiple_sclerosis_lesions"

/dev_stage="Age 46"

/lab_host="DH10B (ampicillin resistant)"

/note="Vector: pT73D (Pharmacia) with a modified polylinker V.TYPE: phagemid; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento

BASE COUNT	117 a	121 c	117 g	114 t	6 others
ORIGIN	Soares and M.Fatima Ronaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH). "				

Query Match	14.7%;	Score 344.8;	DB 87;	Length 475;
Best Local Similarity	92.2%;	Pred. No. 1.8e-80;		
Matches 427; Conservative	0;	Mismatches 27;	Indels 9;	Gaps 6;

OY	1423	tttaaggttccttgagaa-cgcgcagctacaatgtgaagtgctcattcgtgaagattcgcgac-t	1480
Db	464	TTCCAGGTCCTGGAGAGCCGCCGACTTACATGATGNGTTCCTCATCTGMAAGATTCGGCACTT	405
OY	1481	acaagcggcgg-aagcagagggccgtc--atgggagaagaccgtctcccttcaagccagc	1537
Db	404	ACAAGCGCGNMAAAGCAGAGGAGGCCGCCCATGAGGGAAGACCTGTCCTTTACAGCCAG	345
OY	1538	ctttct---aacctggttaactttggtctataagaatgtgtgccagggtctactctgaacggg	1594
Db	344	CCCTTTCTACAACTCGGTATTCTTGGCTATAAGATGTGTCCAGGGGTCACTCGAAGCGGG	285
OY	1595	acgggactgggaaaggagacgacctgtgcgtgttttctcaatgctgtgagaaatg	1654
Db	284	ACGGGATGGGGAAGGGAGCCACTGTGCGCTTTTTCATCAATGCGTGGAGAAATG	225
OY	1655	atgcctctgtctccttgcgctttaagcagaagaatgacactcaatgctg-atgatacaggg	1713
Db	224	ATGCGCTGCTTCCTTCCCTTGCCCTTTAAGCAGAAATGACACTCCTNCTGATGATNACAGGT	165
OY	1714	tcacctgaagctcaatttgggagaatgataaagccagaccccaagaagcagcgactcaag	1773
Db	164	TCCTCTGACGCTCATTTTGGAGATGCACTTAAAGCCGACCCAAAGCAGCAGCTTCAAG	105
OY	1774	aagcccaactggagaagatgaataatcgccctcgtgcctgcagctcttltgtgcccacaactgt	1833
Db	104	AAGCCCACTGGAGAGATGAGATGANTCCTCTGCGTCCGCCAGTCTTGTGTGGCCCAAACTGT	45
OY	1834	ctagaagaatggagacatfatataagaatgatacaattttatata	1876
Db	44	CTAGAAAATGGACATATATTAAAGATGATACATTTTATTA	2

RESULT	13
LOCUS	W40768/c
DEFINITION	W40768 535 bp mRNA EST 11-SEP-1996
ACCESSION	U38411.r1 Soares mouse p3MNF19.5 Mus musculus cDNA clone
VERSION	IM38411.5 similar to gb:U21050 Mus musculus Cd40 receptor
KEYWORDS	associated factor 1 (MOUSE);, mRNA sequence.
SOURCE	W40768
ORGANISM	W40768.1 GI:1325087
REFERENCE	EST.
AUTHORS	house mouse.
	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
	1 (bases 1 to 535)
	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T.
	Geisell,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
	Theising,B., Wylie,T., Lennon,G., Soares,B., Watson,R. and
	Wilston,R.
TITLE	The WashU-HMI Mouse EST project
JOURNAL	Unpublished (1996)
COMMENT	On Jan 7, 1998 this sequence version replaced gi:933067.

This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:222605
 Seq primer: EMP1mer
 High quality sequence stop: 135.
 Location/Qualifiers
 1..335..

BASE COUNT	113 a	150 c	132 g	140 t	
ORIGIN					
Query Match	14.2%	Score 332.8	DB 91	Length 535	
Best Local Similarity	84.5%	Pred. No. 2.9e77			
Matches 399	Conservative 0	Mismatches 67	Indels 6	Gaps 2	

QY	202	tctcttaaatatgagatgtagtaaaataatgactctcttccttcgagcgctctgacataaacccg	261
QY	469	TTTCTTAAGATGAGATATACGAAATAAGATGGATTTCCTGCGACACTGCGCCTTAACCA	410
QY	262	ccgctaaagtctgcacactgacccgagctgctcgtgagcgccaglttttgcctcctaacaaga	321
Db	409	CCCCTAAGCTGCGAGCTGTATCGGGGGCGCAGG---GTCCCTGTCTGTGCGCGGACAAAGA	353
QY	322	ggttaacaaggaagaagtttctgtaagaacgctgtaggaacaagatagaagctgtgagaatgccac	381
Db	352	GGCTACAAAGGAAAGTTTGTAAGAACCGGTGAAGACAAGTACAAAGTCCGAGAAATGCCGC	293
QY	382	ctgtgtcgtctgcagcccgcaagaccgaagtgtgtggagccgcttctcgtcgagaactgcatg	441
Db	292	CTGGTGCGTTCAACCGGAGACAGACGGATGTGGCCACGGTTCTTGCGAGACTGCATG	233
QY	442	gcgagccctgctgagctcttcaagtccaataatgtacacgctgtctaagaagagacatcgttaaa	501
Db	232	GACCCCGCTCGACCTCTCCACATCCAAATATGGACACCGTGGCCAAAGAAACATATCAAA	173
QY	502	gataagtgtttaagagaataatctgtcgaagagaanaattctgctctcttcagatctatgt	561
Db	172	GACAAAGCGTTTAAGATTAATTCGTGCAAGAGAGAGATTTGTGGCCCTTCAAGTCTACTGT	113
QY	562	cggaaatgaagccagaagctgtctgcagagcagttaatctgtggacat---ctgtgtcattta	618
Db	112	CGGATGAAGCAAGAGGTTGTGCGAGACACCTGCTGGAGATCTGCTGTGCACCTA	53
QY	619	aaaaatgatccatttttgagaagacttcagctgtgtgctctctgactgactgcaag	670
Db	52	AAAAATGATGTCAATTGTGAGAACTTCCCTGCTGTGCTGCCGACTGCAAG	1

TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Jan 7, 1998 this sequence version replaced gl:933067.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 404)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Oct 31, 1997 this sequence version replaced gi:1520960.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
www-bio.illn.gov/dbp/image/image.html

FEATURES
source
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
1..404
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:825399"
/clone_id="NCI_CGAP_GCB1"
/issue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, 19D-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAGAGGAGGCGGCTCATTTTTTTTTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT3D vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 104 a 109 c 121 g 70 t
ORIGIN

Query Match 13.1%; Score 305.8; DB 27; Length 404;
Best Local Similarity 98.8%; Pred. No. 3.6e-70;
Matches 329; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 41 ggcagcgacgcgagatgaggaataatgagcccaagaagtatgaccattggttaagt 100
DB 73 GCATCGGACCCCGAGATGAGGAATGAGGCCCAAGAAGTATGATGCTTAAAGT 132
QY 101 cccgagaagatgcagaacacagaccatgagatgagactgctgctcct-gctcc 159
DB 133 CCCAGAGCAGGCAAAATCAGACTGAGATCAGAACTGGCTCTGCTGCTGCC 192
QY 160 tactcttaagagatcgctgctctacagagaagagactcctcttccttaaatgagtcg 219
DB 193 TACTCTTTAAGGATCGCTGCTCTACAGAGAAGAACCTTTCTTAATAATGAGTCG 252
QY 220 agtaaaagatgagactcttcctgagcgctgcagactaacccgcgctaaagctgacact 279
DB 253 AGTAAAGAGATGAGACTCTCTGCGCGCTGACAGTAAACCCCGCTAAAGCTGCACACT 312
QY 280 gaccgcaatgctggagagccagtttttgcctgataaagaggttaacaaagaaagttt 339

DB 313 GACCGCACTGCTGGGACGCCA-TTTTGTCCCTTAACAAGAGGTATACAGAAAAGTTT 371
QY 340 gtaagacacctgtagagacaaatgataagtgtag 372
DB 372 GTGAAGACCGCTGAGAGCAACTACAGAGTGTAG 404

RESULT 15
A1549245
LOCUS
DEFINITION UI-R-C3-1x-d-02-0-UI-s1 UI-R-C3 Rattus norvegicus cDNA clone
UI-R-C3-1x-d-02-0-UI-3', mRNA sequence.
ACCESSION A1549245
VERSION A1549245.1 GI:4466733
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 407)
AUTHORS Bonaldo, M.F., Lennon, G., and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On Jul 19, 1995 this sequence version replaced gi:2939456.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares lab clone distribution: clones will be available through
Research Genetics (www.resgen.com) This clone is also available
through the I.M.A.G.E. Consortium at ILNL (infoimage.illn.gov).
IMAGE ID=1755915 The following repetitive elements were found in
this cDNA sequence: 164-216, >(GGA)n#Simple_repeat
Seq primer: M13 Forward
POLYA-NO.

FEATURES
source
Location/Qualifiers
1..407
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C3-1x-d-02-0-UI"
/clone_id="UI-R-C3"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2p,
UI-R-C1, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-C3) was constructed as follows: PCR amplified
cDNA inserts from UI-R-C2p clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the UI-R-C2p library in the form of single-stranded
circles. The remaining single-stranded circles (subtracted
library) was purified by hydroxyapatite column

chromatography, converted to double-stranded circles and electroporated into DH103 bacteria (Life Technologies) to generate the UI-R-3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, *Genome Research* 6:791-806, 1996).

BASE COUNT	122 a	82 c	105 g	98 c
ORIGIN				

```

Query Match      9.1%;   Score 213.6; DB 41; Length 407;
Best Local Similarity 84.2%; Pred. No. 8.8e+46;
Matches 330; Conservative 0; Mismatches 39; Indels 23; Gaps 7;

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QY	1868	cttcttaataagatcatagctggaactctcgatctggtccgatccctcgataaagtaagctg	1927
Db	13	TTTTTTTTAAAGTATAGTGGATACCTCGGATCTGGCTTACCCCTGACAAAGAACAGG	72
QY	1928	aggctgatttagcaagaagcaactcctctctgaggatttgaacggtctgtcttccactgag	1987
Db	73	AGCTGATTTCAGCAGAGGATACCTCTGCGGGG - GTTGACAGGCTCTTTCACGAG	131
QY	1988	gtcctcgctcagaaaaaggaacctgtgagacggagggaagcggcgaagcggaagcg -	2045
Db	132	GTCTCGCCCTCAG - AAAGGACCTTGTGGACACAGAGAACACCCGGAAGGAGAGGA	190
QY	2046	-----tgccggcgaggagagcagcgagagacaca---cctgacagtttita	2091
Db	191	GGAGGTCGAGTGGCTGGGAGAGAGACCCACATGTGMAAAGAACCCCAAGCGATTTTATA	250
QY	2092	atagactagccacacttcactctgaagaattattatctcctcaacaagataaatctgt	2153
Db	251	ATAGACTACCCACAC - TCACCTGACAGATATTATTATCCATCAACAAGATTAATATGCT	309
QY	2152	gtcagaagaggttctcatttcaattttaaagactcagtaattaaagtggaacaatat	2211
Db	310	GTGAGGAAGGATTTTCATTTCATTTTAAAGATCTTGTTAATTAAGTGG - AAACATAT	368
QY	2212	atgctaaacaagaacaatgatttttcttc	2243
Db	369	ATGCTA---AAAGAAACATGATTTTCTTTC	397

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Search completed: September 2, 2000, 09:01:32
-Job time: 7559 sec
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KW		Cd40 receptor associated factor 1; CRAFL; TRAF-3; p70; p5; p15;
KM	p55; p55delta9; p70delta9; p55delta9_10; p70delta9_10; p55delta8_9;	
KV	p80delta8_9; human; CD40 mediated intracellular signalling;	
KW	organ rejection; allergy; hay fever; autoimmune disease;	
KV	rheumatoid arthritis; systemic lupus erythematosus;	
KW	myasthenia gravis; idiopathic thrombocytopenia purpura;	
KM	'Graves' disease; hemolytic anaemia; diabetes mellitus; psoriasis;	
KW	hyper immunoglobulin E syndrome; apoptosis; infectious disease;	
KV	Richter's syndrome; spondyloarthritis; Lyme disease; HIV; syphilis;	
KW	tuberculosis; arthritits; scleroderma; fibrosis; pulmonary fibrosis	
KM	pneumoclonosis; adult respiratory distress syndrome; pneumonitis;	
KW	asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;	
KM	atherosclerosis; multiple sclerosis; glomerulonephritis;	
KW	glomerulosclerosis; glomerulopathy; kidney disease; nephropathy;	
KM	endocarditis; leprosy; malaria; Goodpasture's disease;	
KW	Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;	
KM	Wegener's granulomatosis; cryoimmunoglobulinaemia;	
KW	Waldenström's macroglobulinaemia; amyloidosis; Sjögren's syndrome;	
KV	bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;	
KW	Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;	
KR	gene therapy; diagnosis; ds.	
OS	Homo sapiens.	
FH	Key	
FT	exon	Location/Qualifiers 1..309
FT		/+tag= a
FT		/number= 1
FT	exon	310.. .517
FT		/+tag= b
FT		/number= 2
FT	exon	518.. .657
FT		/+tag= c
FT		/number= 3
FT	exon	658.. .918
FT		/+tag= d
FT		/number= 4
FT	exon	919.. .971
FT		/+tag= e
FT		/number= 5
FT	exon	972.. .1076
FT		/+tag= f
FT		/number= 6
FT	exon	1077.. .1244
FT		/+tag= g
FT		/number= 7
FT	exon	1245.. .1325
FT		/+tag= h
FT		/number= 8
FT	exon	1326.. .1400
FT		/+tag= i
FT		/number= 9
FT	exon	1401.. .1493
FT		/+tag= j
FT		/number= 10
FT	exon	1494.. .1634
FT		/+tag= k
FT		/number= 11
FT	exon	1635.. .1809
FT		/+tag= l
FT		/number= 12
FT	exon	1810.. .2381
FT		/+tag= m
FT		/number= 13
FT	CDS	169.. .2384
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FT		//product= p70 (CRAFL-b, p77 isoform)
FT	CDS	/note="no exon 3 in p70-1 coding sequence"
FT		169.. .559
FT		//+tag= o
FT		//product= p5
FT		/note="no exon 2 in p5 coding sequence"
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FT		

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FT      CDS      /product= p15
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FT      /note= "no exons 9 or 10 in p70del9,10 coding
FT      sequence"
FT      CDS      /tag= s
FT      /product= p70del8,9
FT      /note= "no exons 8 or 9 in p70del8,9 coding
FT      sequence"
FT      CDS      /tag= t
FT      /product= p55 (CRAF1-a, p60 isoform)
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FT      /product= p55del9
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FT      CDS      /tag= v
FT      /product= p55del9,10
FT      /note= "no exons 9 or 10 in p55del9,10 coding
FT      sequence"
FT      CDS      /tag= w
FT      /product= p55del8,9
FT      /note= "no exons 8 or 9 in p55del8,9 coding
FT      sequence"
FT      PD        WO9734473-A1.
FT      PD        25-SEP-1997.
FT      PF        21-MAR-1997. U05076.
FT      PR        18-SEP-1996; US-026584.
FT      PR        21-MAR-1996; US-013820.
FT      PR        01-MAY-1996; US-016626.
FT      PR        01-MAY-1996; US-016659.
FT      PA        (UNCO ) UNIV COLUMBIA NEW YORK.
FT      PI        Cleary AM, Frank DM, Lederman S;
FT      PI        WPT: 97-479907/44.
FT      DR        P-PSDB; W27428-37.
FT      PR        Protein comprising CRAF1-b domain capable of inhibiting CD40
FT      PT        mediated cell activation - useful to treat conditions characterised
FT      PT        by aberrant or unwanted level of CD40 mediated intracellular
FT      PT        signalling
FT      PS        Example 1: Fig 1A-P; 158pp; English.
FT      CC        This 2918 bp cDNA sequence encodes CRAF1 (TRAF-3) and its deletion
FT      CC        and alternative splice isoforms (see W27428-37). It is derived
FT      CC        from several cDNA species from a Raji B cell library. CRAF1
FT      CC        peptides, comprising from 0-4 zinc finger domains, and nucleic
FT      CC        acids encoding them, can be used to inhibit CD40 ligand activation
FT      CC        of cells that express CD40 on their surface, particularly by
FT      CC        introducing the nucleic acid molecule into the cells, useful to
FT      CC        treat conditions characterised by an aberrant or unwanted level of
FT      CC        CD40 mediated intracellular signalling, such as organ rejection in
FT      CC        a subject receiving transplant organs, or a CD40 dependent immune
FT      CC        response in a subject receiving gene therapy. The condition may be
FT      CC        an allergic response, an autoimmune response, or may be dependent
FT      CC        on CD40 ligand-induced activation of epithelial cells, an
FT      CC        inflammatory kidney disease, a smooth muscle cell-dependent
FT      CC        disease, or a condition associated with Epstein-Barr virus. CRAF1
FT      CC        nucleic acids can also be used as probes in diagnostic testing.
FT      CC        The gene for CRAF1 is located on human chromosome 14q32.2.
FT      SQ        Sequence 2918 BP; 768 A; 728 C; 822 G; 600 T;

Query Match          97.6%; Score 2282.2; DB 1; Length 2918;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2322; Conservative 0; Mismatches 8; Indels 5; Gaps 3

```


Oy	1378	atgtctagtgatgcaacgacatccgccttaagccgacatgagcttgcgtccaaagtccttgcag	1437
Db	1321	ATGTCTGATGTGCACGACATCCGCTTAGCCGACATGACACTGGCTTCCAGGTCTCTGAG	1380
Oy	1438	accgcacgactcaatctgaagtgctcatctctgaaagattcgcgactatacaacgycggaagacg	1497
Db	1381	ACCGCACGCTACATATGGAGATGCTCATCTGTGAATATCGGACATACAAAGGCGGGAAGAG	1440
Oy	1498	gaagccgctcatatggyggaagaccctgtccctttacagccagcccttttaacgtgttaacttt	1557
Db	1441	GAGGCGCTGCATGAGGGGAAGACCTGTCCCTTTACAGCCAGCCTTTTACACTGTGTACTTT	1500
Oy	1558	ggctataaagatgtctgcacaggtcttaacttaacgcyggaacggaatggygaagagacac	1617
Db	1501	GCTATATAGATGTCTGCCAGGGTCTACTTAAAGGGGACGGATGGGAAAGGGACGCAC	1560
Oy	1618	ttgtcgcgtgtttttgtcatcatatgctgtgaaataatgatagccctgtcttccctgtgcgcttt	1677
Db	1561	TTGTGCGGTGTTTTTGTCTCATCATGCGGAGAAATATGATGATGACCTGTCTTGGCGGTTT	1620
Db	1621	AAGCAGAAAGTGAACACTACGTGATGTGAACAGGGGCTCTCTGACGTATTTGGAGAT	1680
Oy	1738	gcatccaagcccgagcccccacacagacagatctaagaagaacccacctggaagataatcatc	1797
Db	1661	GCATTCCAGCCCGACCCCAACAGCAGCAGCTTTAAAGAACCCACTGGAAGATGATATCT	1740
Oy	1798	gcctctgctgtcccaagctctttgtgcccacaactgtctctagaanaatlygacataataa	1857
Db	1741	GCCCTGTGGCTCCCAAGCTTTGTGGCCCAACTGTCTAGAAAATGGGACATATATTTAA	1800
Oy	1858	gatgatacaatttttatataagtcataatgtatgtatcttggtatctgcgcgaatccctgataa	1917
Db	1801	GATATATCAATTTTTATTTAATAAGTCATAGTGAATCTTGCGATCTGCCATCCGTGAATA	1860
Oy	1918	gtagctgggagagtgatgatttagacgaagcaactccctctgggagatttgaaccggtctgt	1977
Db	1861	GTACTGTGGGAGGTGGATTTTAGCAGAAAGCACTCCTCTGGGGATTTTAACGGGTCTGT	1920
Oy	1978	cttcactgaagttctctgcgctcaganaaagacctgttgagaacgaggaacgycagaaag	2037
Db	1921	CTTCACTGAGGTCTCTCGCGCTCAGAAAAGGACCTTGAGAGACGAGAGAGCGGAGAAAG	1980
Oy	2038	cgagacgctgacgagcggaggaagagccacacgagagacacactgacacagtttataatagac	2097
Db	1961	CGGACGGGTGCGCGGGGAGGAGGCCAGCGCTGAGCACACTGACACAGTTTATATATGAC	2040
Oy	2098	tagcacacacttcaactctgaagaatattatctctcaacagaataataattgctcagaa	2157
Db	2041	TAGCACACTTCACACTGAGAGATATATTATCTTCAACAAGATAATATTCGTCTGAGA	2100
Oy	2158	gaaggtttcaatttcaattttaaagatctagtiataatgaagtlygaaacatatatgcta	2217
Db	2101	GAAAGTTTTCATTTTTCATTTTAAAGATCTAGTATTAATTAAGGGGAAAACATATATGCTA	2160
Oy	2218	aacaaagaacaacatgattttttctctccttaacttgaacacccaaaaaa--aacacacaca	2275
Db	2161	AACAAAAGAAACATGATTTTCTTCTCTTAACCTTGAACACCAAAAAAACACACACACA	2220
Oy	2276	cacacacgttgggatacgtgcgacatgtcagcatgtttaagttaaaaggaagattatgaaat	2335
Db	2221	CACACACGTGGGATGACTGGACATGTACACATGTTAAGTAAAGAGAGATTAATGAAAT	2280
Oy	2336	agta 2339	
Db	2281	AGTA 2284	

AC	23-MAR-1998	(first entry)	-	CD40 associated protein (CAP)-1 encoding DNA.
DE	CD40 associated protein (CAP); agonist; gene therapy;			
KM	cell proliferation; treatment; cancer; autoimmune disease; ss.			
OS	Homo sapiens.			
FN	Key	Location/Qualifiers		
FT	CDS	137..1768		
FT		/tag=	a	
FT		/note=	"CAP-1 protein"	
PN	W0616665-A1.			
PD	06-JUN-1996.			
PF	04-DEC-1995; U15695.			
PR	02-DEC-1994; US-349357.			
PA	(LJOL) LA JOLLA CANCER RES FOUND.			
PI	Reed JC, Sato T.			
PI	WPI; 96-286818/29.			
PR	P-Psdb; R98833.			
PT	New CD40 associated protein, agonists and antagonists - used to			
PT	modulate cell proliferation, immune response, apoptosis etc., e.g.			
PT	for treating cancer or autoimmune disease			
PS	Claim 13; Fig 1; 94pp; English.			
CC	This DNA encodes a CD40 associated protein (CAP)-1. The CAP is a protein			
CC	that specifically binds to CD40, a cell surface receptor involved in			
CC	apoptosis. Agonists and antagonists of CAP can increase or decrease			
CC	the level of CAP expression in a cell and can thereby modulate the			
CC	function of the cell. Such compounds can be used to treat cancer,			
CC	autoimmune diseases like asthma, hay fever, rheumatoid arthritis and			
CC	immunodeficiency diseases and neurodegeneration. Antibodies that bind			
CC	specifically to CAP can be used to assay CAP, to detect pathologically			
CC	altered levels. This nucleic acid can be used to identify related genes			
CC	and to express CAP for gene therapy.			
SQ	Sequence 2240 BP; 637 A; 510 C; 604 G; 489 T;			

CC The present sequence encodes murine TRAF5 a protein of the tumour
CC necrosis factor (TNF) receptor associated factor family. TRAF5
CC products can be used in immunisation, to treat allergies and as
CC cell proliferation inhibitors. They can also be used to screen for
CC TRAF5 inhibitors or regulators. They can also be used to screen for
SQ Sequence 2105 BP; 540 A; 530 C; 578 G; 457 T;

Query Match 15.3%; Score 358; DB 1; Length 2105;
Best Local Similarity 55.0%; Pred. No. 8,1e-88;
Matches 876; Conservative 0; Mismatches 695; Indels 21; Gaps 8;

327 caaagaaagatttgaagaccgtgagagacaagatgtagaagtgccacctgt 386
280 CGAGTACCAAGTGTGGACAGCTGGAGAACGCTCAATATGCTTGCACCTCCGT 339
387 gctgtgacccgagacagacagagtggtgagacacgctctgacagagtgtagc 446
340 GCTTCAACACCCACCAACAGCGCTGGCGACCCCTTCTGCACAGAGTCCGCTC 399
447 cctgtgagct---ctcaagtcacaaatgtaacagcgtgtcaagagagatcgtaaga 503
400 TCTGAAGAAATTCATTCGGTGGCGATCTGCCGTTAGCAAGAGAGTCAAGCTCA 459
504 taagtgttaagataatgtctgacagagagaataatctgctcttcacatctatgtcg 563
460 GGGAGGTGTTCAAGACACTGCTGCAAAAGAGTTCATTAATTCACAGTCTACT--G 516
564 gaatgaagacagaggtgtgacagagacgttaatcgtgagacatctgtcatltaaaaa 623
517 CAAAAACGCCCCGGGTGCATCCAGATTAATTCGGACGATTCAGAGAACCACTTCA 576
624 tgatgcatltagaagacatccatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 683
577 GCACCTGCTCTTCCAAAGCCGCTGCCCTGACCTTAACGAGAGCTGCCGGAGCCAT 636
684 gaaagccctgacagacagtgtagaagagtgtagaataacagagagacacagtcagcca 743
637 GAAAGAGTGAAGAGACCTGAGCCGATCTCCGCTTCCAGAGAGAGAAAGTCCCTTA 696
744 ctgcaagagtcaggttccgatactgacgtgtgacagaaacagagacacagcagtcctgt 803
697 CTGCAAAAGGAGATAGTGTGTGACCAACCTGAGCATGAGAGAAACCTGCTCCTCG 756
804 cgt 863
757 GTACCCAGT 813
864 tgacacactgtcagagtggtgtcaatgtccccacacgtgtgtgtgtgtgtgtgtgtgt 923
814 TGAACACCTTACTGTATGTCTGTGCTGTGAGCAAGACTGTCCCTTTAAGCACTATGCTG 873
924 cgttttccaggggacaaacacagacagatcaaggtccacagagcagctcgcgtgtgacga 983
874 CACTGTAAAGGTAAGCGGGGGAACCTGTGTGAGCATGAGCGGACACCTTGCAGAGCA 933
984 cgtcaacctgtcgaagagtgtagcaactcgtctcgaagaagaagtggttccctgtgtcgaa 1043
934 CATGCTTCTGT 993
1044 tgaagagtgtagaagaagaagaagacatcaaaagtgtgacaatcagatgtagcttga 1103
994 GAGTCTGAAACAGAAAGAAACAGATCCAGACAGCTGGCAGAAACCGTGAAGAGTTCGA 1053
1104 aattgaatitgagagacaaagaagaatgcttgaataatgaatgaatccaaatcccttcat 1163
1054 AAAGAGACTTAAGCAGTTACACAGATGTTTGCAGAAATGAGACTTTCCTCTCAATATGT 1113
1164 acagcagtgtagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1223
1114 CCAG---GCTTCAACAGGTACACAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1170
1224 ctccgcagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1283

1171 GCTGTACA-AATAGTTACACAGCCACCACTGCACTTGAATCTAGGCTTTGGT-GGAT 1228
1284 ccgctgacccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1343
1229 GCGGTGACACGCTGAACAGAGATCACCCAGCTGAGAGCAGAGTAC-CAGAGATTAAGT 1287
1344 cctgtgtgagtcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1403
1288 TCTTTTAAGGGGGAGACCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1347
1404 agccagacatgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1463
1348 GAATTAAGACAGAGAGCGCTTTAAGCAGTGTGAGAGCGCCCTGCTACATGAGCAGCTCAT 1407
1464 ctgagaagattcgcagacatacaagcagcagcagcagcagcagcagcagcagcagcagcagc 1523
1408 CTGGAAGGTGACAGATACAGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1467
1524 ccttaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1583
1468 CCTTTCAGCCAGCCTTCTACACAGCCGCTGCGCTACCGGCTTCTGTCAGAGGCGCTA 1527
1584 cctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1643
1528 CTTGAAGGGGAGCGGGGTGGGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1587
1644 tggagaataatgacccctgt 1703
1588 CGGTAGTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1647
1704 ggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1763
1648 GACACAGAGCGGCAAGAGAACCATATGTGTGAGACCTTCAAGAGTGAAGCCCAAGAGAG 1707
1764 cagcttcaagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1823
1708 CAGCTTCAAAAGCCAGAGAGCGGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1767
1824 ccaactgttctaga-----aaatgggacatatataaagaatgataatltatataa 1877
1768 GACCTTACTGTGAGAACTCCAGAGAACCTTACTTAAGAGCAGACACTGTCTTGAA 1827
1878 agtcatagtgatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1909
1828 AGTGCGCGTGTGATTAAGTACTGAGTGTGAGATC 1859

RESULT 6
T87039
ID T87039 standard; cDNA to mRNA; 2254 BP.
AC T87039:
DT 18-MAR-1998 (first entry)
DE DNA encoding murine TRAF5, a novel TNF receptor factor family protein.
KW TRAF5; tumour necrosis factor receptor; TNF;
KW TNF signal transducer system; ss.
OS Murine sp.
FH Key : Location/Qualifiers
FT CDS 323..1999
FT /tag= a
FT PN WO9731110-A1.
PD 28-AUG-1997.
PF 24-FEB-1997; J00512.
PR 22-FEB-1996; JP-034674.
PA (SUME) SUMITOMO ELECTRIC IND CO.
PI Nakano H, Nakata M, Okumura K, Yagita H;
DR P-PSDB; W29257.
DR P-PSDB; 97-435162/40.
PT Tumour necrosis factor receptor associated factor family protein.
PT TRAF5 - useful to study signal transduction in tumour necrosis
PT factor receptor family
PS Claim 2; Pages 44-46; 69pp; Japanese.
The present sequence encodes a novel protein, designated TRAF5, which is

CC a member of the tumour necrosis factor (TNF) receptor associated
 CC family. The TRAF5 protein has a coiled-coil domain, a leucine
 zipper motif and binds to lymphotoxin beta receptor and to CD30, but not
 CC to CD40 or TNF receptor 2. TRAF5 and its corresponding DNA are useful for
 CC the investigation of the signal transducer system of the TNF receptor
 CC family and the functions of TRAF proteins. They can also be used as
 CC probes for research and diagnostic purposes, and investigation of the
 CC specific applications of potential therapeutic agents.
 SQ Sequence 2254 BP; 581 A; 576 C; 625 G; 472 T;

Query Match 15.38; Score 358; DB 1; Length 2254;
 Best Local Similarity 55.0%; Pred. No. 8.4e-88;
 Matches 876; Conservative 0; Mismatches 695; Indels 21; Gaps 8;

CC 327 caaggaagaatttctgaagacccgtgagagacaagtaacagtgtggaagtcacccctgt 386
 DB 415 CGAGTACACAGTTTGTGGAGAGTGGAGAACGCTACAAATGTGCTTCCACTCCGT 474
 CC 387 gctgtgacgcccgaagacagccagtggtggcaccgctctggcgagagctgagtcggcg 446
 DB 475 GCTTCACACACCCCCACACAGCCGCTGCGGACCGCTTGTCCAGCATGCTCCGTC 534
 CC 447 cctgtgagct--ctcaagtcacaaatgtacagcgtgtcaagagagcatgttaaga 503
 DB 535 TCTGAGAAATTTGAACCTGGTGGCGATCTGCCGCTAGACAAAGAGTCATCAACCTCA 594
 CC 504 taaggtgttaagataatctgtcgaagagaaattctgtcttcacatctatgtcg 563
 DB 595 GGAGGTGTTCAAGACAACTGCTGCAAAAGAGAAATTTCAATTAACAGCTTACT--G 651
 CC 564 gaatgaagacgaggtgttcagagcaagtaatgttggaactctggtgcatttaaaa 623
 DB 652 CAAAAACGCCCCGGGTCAATGCCAGATTAATCTGGAGCATTCAGAGACACCTTCA 711
 CC 624 tgattgcaatttgaagaaacttcaatgtgtcgtcctgactgacaaagaagatctgag 683
 DB 712 GCACTGTTCTTCCACAGCCGTGCTGCTGCCCTTAACAGAGATGCGGGAAGCATCTCCG 771
 CC 684 gaaagacctgcgagacacagctggaagagcgtytaataacgggaagacacatgacga 743
 DB 772 GAAAGACCTGGAAGAGCAGCTGAGGCGCATACGCGGTCCGAGAGAGAAATGCTTTA 831
 CC 744 ctgcaaggtcaggttccgcatgagtcgctgagaaacagaaagacacagctgtccctg 803
 DB 832 CTGCAAAAGGACATAGTGTGACCAACCTGAGGATCATGAGAAATCTGTGCTGTC 891
 CC 804 cgtgtgtgtcctgcctcacaagctgacagctcaccagctcctgagagagctgtgag 863
 DB 892 GTACCCAGTGTGTCTCCACACAGSTG---TGTGACAGCTATTCACAAAGCTAGGCTGA 948
 CC 864 tgcacactgtcagaagtgltcaatgtcccccagcacctgttaagcgtcatgtctg 923
 DB 949 TGAACACCTTACTGTATCTCTGAGGCTGAGCAAGACTGTCCCTTTAAGCACTATGCGTG 1008
 CC 924 cgttttcaagggaacaaaccagcatcaaggccagagagcactcgcgcgtgtcagca 983
 DB 1009 CACTGTCAAGGTTAAGCGGGGAACCTTCTGAGCATGAGCGGCAAGCCCTTCAGAGCA 1068
 CC 984 cgtcaacactgtcgaagaggtgtgagcaactcgtcgaagaagaggttccctgtgagaa 1043
 DB 1069 CATGCTTGTGTTTGAAGAGAACTACCACTAAGACAGCGGATCTGATTTATATCA 1128
 CC 1044 tgaaggtgagaaaaaacaagagacatacaaaattgtcacaactcagatatgtagcttga 1103
 DB 1129 GAGTCTCAACAGAGAAAGCAAGATCCAGCTGGCAAAACCGTGAAGAAATTTGCA 1188
 CC 1104 aattgaatttgagagacaaaaggaatcttctgaataatgatccaaatctcattt 1163
 DB 1189 AAAGAGCTTAAGCAGTTTCAACAGATGTTTGGAGAAATGGAATTTTCTCAAAATGT 1248
 CC 1164 acagagagtgatagacagcccaagcagagagaaactgaagagctgtgcaagagatccgggc 1223

DB 1249 CCAG---GCTCTCACAGTACACGAGCAAGTACAGTGTGCTGGAGCGCAGTGGCGCA 1305
 CC 1224 ctccgagagacttggagagagacagaaagcatgaagagcagctgtgtccctccagaa 1283
 DB 1306 TCTGTATAA-AATAGTTTAAACAGAGCCAAATGCACTTGATCTGAGGCTTTGGT-GGAT 1363
 CC 1284 ccggtgtacagcagctggagagcgttgagacagagcgggagagagtggtgtcgaacagag 1343
 DB 1364 GCGGTGACACCGTGAACACAGAGATCACACAGCTGGAGAGCCAGTGAAC-CAGAGATTAGT 1422
 CC 1344 cctgtgagtcaccaagcagtcgagccgcatgacacagatgtcgtgagtgacagacatccgct 1403
 DB 1423 TCTTTAGAGGGGAGACCCACCAAGCAGACACATTAATATTCACAAAGCACACAT 1482
 CC 1404 agccgacatgacactgtgtgtcccggtctgtgagacccgacagctcgaatgtgactat 1463
 DB 1483 GAATTAAGAACAGAGAGCGGTTTAAGCACACTGAGAGGCCCTGTCTACATGTGCAACCTAT 1542
 CC 1464 ctggaagatcgcgactacagcggcggaagcagagagccgtcatgtgggaagacccctgtc 1523
 DB 1543 CTGGAAGTGAACAGATTACAGGTTGACAGAGAGAGAGGCCCTGGAGGGCACACAGTCTC 1602
 CC 1524 cctttacagcagcccttctcactgactgttacttggctataagatgtgtgccaaggtcta 1583
 DB 1603 GGTCTTCAAGCCAGCTTCTTACACACAGCCGCTGCGGCTACCGGCTGTGCGCAGGGCGTA 1662
 CC 1564 cctgaacgggagcggatgtggagagagggagcgaactgtcgctgttcttctcatatcg 1643
 DB 1663 CCGTAACGGGAGCGGCTGGGGAAGGAGAACGACCTGCTCCCTGTCTTGTGTGATCG 1722
 CC 1644 tgggaatgatgtgcctgtcctgtcctgttgaagagaaagtgaacatcatgtgat 1703
 DB 1723 CGGTGATTTGACTGCTGCTGCTGCACTGCGCTGTTACGAGAGAGGTGACCTGATCTTTT 1782
 CC 1704 ggaacaggggtcctctcgaactcatttggagatgtcattcaagcccgaccccaacagag 1763
 DB 1783 GGACAGAGAGCGGCAAGAAAGAACATATTGTGAGAGCCTTCAAGCTGACCCCAAGCAG 1842
 CC 1764 cagctcaagaagcccaactgtgagagatgaatctgcctcgtgtgtccagtcctgtgtgc 1823
 DB 1843 CAGCTTCAAAAGGCCAGATGCGAGATGACATTCCTGCTGCTGCCGCTTTGTGTGC 1902
 CC 1824 ccaactgtctaga-----aaatggagacatatgaagatgttaaatlttataa 1877
 DB 1903 GCACCTTCTCTGAGAACTCCAAAGAACCTACTATTAAAGGACACACTGTTCTTGA 1962
 CC 1878 agcatagtgatacttcgactcgtcccgatc 1909
 DB 1963 AGTGGCCGTGATTTAACTGACTTGGAGATC 1994

RESULT 7
 T87040
 ID T87040 standard; cDNA to mRNA; 2846 BP.
 AC T87040:
 DT 18-MAR-1998 (first entry)
 DE DNA encoding human TRAF5, a novel TNF receptor factor family protein.
 KW TNF signal transducer system; ss.
 OS Homo sapiens.
 FH Homo
 FT CDS Location/Qualifiers
 FT CDS 100..1773
 FT /*tag= a
 FN WO9731110-A1.
 PD 28-AUG-1997.
 PF 24-FEB-1997; J00512.
 PR 22-FEB-1996; JP-034674.
 RA (SOME) SUMITOMO ELECTRIC IND CO.
 PI Nakano H, Nakata M, Okumura K, Yagita H;
 DR WPI; 97-435162/40.
 P-PSDB; W29258.
 PT Tumour necrosis factor receptor associated factor family protein,
 TRAF5 - useful to study signal transduction in tumour necrosis

factor receptor family.
 PS Disclosure: Pages 49-52; 69p; Japanese.
 CC The present sequence encodes a novel protein, designated TRAF5, which is
 a member of the tumour necrosis factor (TNF) receptor associated
 factor family. The TRAF5 protein has a coiled-coil domain, a leucine
 zipper motif and binds to lymphotoxin beta receptor and to CD30, but not
 to CD40 or TNF receptor 2. TRAF5 and its corresponding DNA are useful for
 the investigation of the signal transducer system of the TNF receptor
 family and the functions of TRAF proteins. They can also be used as
 probes for research and diagnostic purposes, and investigation of the
 specific applications of potential therapeutic agents.
 SQ Sequence 2846 BP; 874 A; 538 C; 637 G; 797 T;

Query Match 13.4%; Score 314.2; DB 1; Length 2846;
 Best Local Similarity 53.4%; Pred. No. 8.6e-76;
 Matches 851; Conservative 0; Mismatches 718; Indels 26; Gaps 8;

335 agttgtgaagacgctggaagacaagtacagtgtagaagtgcacactgtgtgtgtca 394
 152 agttgtgagcgttggaagacgctacaaatgtgcttgcctgctgctgcttccaca 211
 395 gcccgagagacgagctgtgtgacccgcttctcgaagctgtcatgtgctgtctga 454
 212 acccccacacagacagatgtggcagccgcttctccacagacatgcatccctgagag 271
 455 gct---cttcaagtcnaaaatgtacagcgtgtcaagagagacatcgttaagaagtgt 511
 272 aatttaaacacagtcgaactcctcctgtagatgaagagctcatcaaatctcagaggttt 331
 512 ttaagatattgtcgtgaagagaagaattctgtccttcaagatcattgtcgaatgaa 571
 332 ttttaagacattgttgcaaaagagagcttcaacttattatattatgtacacaaatgcc 391
 572 gaagaggtgtgtcagagcagcttaagtgtgacatcgtgtgcatttaaaatgtatgcc 631
 392 ctggatgtatgc---caggtttatctgtggcgggtraccagatcacttgcagatgct 448
 632 atttgaagaacttccatgtgtgtcgtcgtcgtcaagaagaagtcttgaagaaagacc 691
 449 tttttcaacctgtgcagctgttcttaagagagtgccggagacagctcctacgaaagacc 508
 692 tgcgagacacgtgtgagagagcgtgttaatacagagagacacacacacacacacac 751
 509 tgaagacattgttgagctgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 568
 752 gtcaagttcgaatgtatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 811
 569 aggatgtgtagatcattcattcattcattcattcattcattcattcattcattcattc 628
 812 tgtctgtccctcaagaatgtcagcgtcctcctcgtgagagcgtgtgagtgacacact 871
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 686 tggcttattgtctctgaagctgacagacagactgctttttaagcactatgtgctgttaa 745
 932 agggagacaacacagacatcaagagcccaagagcagctccgcgtgtcagcagctaac 991
 746 cggatgaagagagac 805
 992 tgtgtgaagagtgtagaactcgtcgtgaagaagagtttctgtgtcgaagaatgaagtc 1051
 806 tgggttttgaagaaatgtcatttgaagaaacagattttgtgactttacacaaagcctag 865
 1052 taagaaaaaacaagacatcaaaagtttgcacaatcagatgtatgttgaattgaatga 1111
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 1112 ttagagagacaaagaaatgtcgtcgtgaataatgaatccaaatccttcaattcagcgag 1171
 926 tcaagacagtttgcacagttgttgccaaaatgaagcttctcccaaacatccag---g 982

1172 tgatagcagcccaagcagagaactgaagagcttgacaagagatccggccctccggc 1231
 983 tttttgacacattgacaaatgacatgcttgctagagctcagagctatattttatc 1042
 1232 agaacctggagagagcagacagcagcagcagcagcagcagcagcagcagcagcagc 1291
 1043 aaa---tggttaacacagacacacacacacacacacacacacacacacacacacac 1098
 1292 ccgagctggagagcgttgagacagagcggggccaa-gtgcctggagacagcgcgtgtg 1350
 1099 gatcacgtaaacacagaaatattaccctctagaaaacatgatatcaaatattagcgttta 1158
 1351 gattccagctgtgagccgagctgacagatcgtgagtgtagcagacatccgctaacccgac 1410
 1159 gaagagaaacttaacaaacatgataccacacatttatttataaagacacagctgagtaa 1218
 1411 atgacctgtgcttccagctgtcgtgagacccgacacacacacacacacacacacacac 1470
 1219 aatgaagagcattttaaactgctgagaggtactgtatattgaagacacacacacacacac 1278
 1471 atcgagactacaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1530
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 1339 acccagcttcttctac 1398
 1591 gggagcggagatggagagagagcagcagcagcagcagcagcagcagcagcagcagcag 1650
 1399 gggagtggtgag 1458
 1651 tatgatgctgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1710
 1459 tttgactactgtgtgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1518
 1711 ggtcctcgtcagcttcaatttggagatgacatcaagccagcccaacagcagcagcttc 1770
 1519 agtgc---aaagaaacattatgagacacacacacacacacacacacacacacacacac 1575
 1771 aagaagccacactggagagatgaatagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1830
 1576 aaagacactgagtgag 1635
 1831 gtccagaagaatggga-----catatataagatgatacatattttatgaagtcata 1884
 1636 gtttggagaaatggcagaaagacacacacacacacacacacacacacacacacacacac 1695
 1885 gtgatactcgtgactgtcccgatccctgataagt 1919
 1696 gtgacttaacagac 1730

RESULT 8
 ID T88023 standard; cDNA to mRNA; 3993 BP.
 AC T88023;
 DT 27-APR-1998 (first entry)
 DE Human TRAF5 cDNA.
 KW Human; TRAF5; tumour necrosis factor; TNF; allergy;
 KW receptor associated factor family; immunisation; treatment;
 KW cell proliferation inhibitor; screening; inhibitor; regulator; ss.
 OS Homo sapiens.
 FH Key
 CDS . 55..1728
 FT . /tag-2
 FT . /product= TRAF5
 PN W09738099-A1.
 PD 16-OCT-1997.
 PF 10-APR-1997; J01236.
 PR 25-DEC-1996; JP-355847.
 PR 11-APR-1996; JP-113035.

QY	1451	atgagaggtccatctggaagaattcgcagactcaagaagcggggaagcgagggcgctcaatc	1510
Db	1004	ATGGCGTGTCAATCTGGAAATTTGGCAGCATATGAGCGGGGGCTACAGAGAGGCCCAAGGCCA	1063
QY	1511	ggaaagaccctgtccctttaagccagccctttcaacatcgttactcttgcttaataatgt	1570
Db	1064	AGCCCAACCTTGAAGTGGCTTCAAGCCACAGCCTTTACACACATAAATGATGGTTACAAAGCTGC	1123
QY	1571	gtgccaaaggtctaaccttgaacgaggagacggagatgggaaaggagacgcactgttcgcgtttt	1630
Db	1124	AGGTGTCTGCAATTCCTCAATGGCAATGGCAGTGGTAGGGCACACACCTCTCATGTACAA	1183
QY	1631	ttgtcatcaatgcgtggaggaatgatgatagcctgttctcttgcgcgttttaagcgaagaatga	1690
Db	1184	TTTCGTGTGCTCCCGGTGGCTCTTGAACATCTCTTGAATGGGCCCTTGGCCCGCCGTGCA	1243
QY	1691	caactcaatcgtatgatgacacaagggttcctct-----cgacgtcatttggagatg	1738
Db	1244	CCCTTCCTCCCTGCTGGATCAAGAGGACCTTGCGTGCTAAACACAGCAGTCACTAGGA	1303
	1739	catcaagaaccgacccaagaacagcagcgtcttaagaagcc	1778
	1304	CTTTCACCCCGACCCAAACTGGAAATTTCCAGAAAGCC	1343

CC	sequence	2248 BP;	635 A;	512 C;	515 G;	586 T;
CC	TRAF6.					
CC	detect TRAF6 homologues and analogues, and therapeutically to					
CC	modulate cellular expression, or intracellular concentration of					
CC	TRAF6.					
CC	DNA encoding tumour necrosis factor receptor associated factor 6 -					
DR	p-PSDB: W32113.					
PI	WPI: 97-535866/49.					
PI	Goeddel DV, Xiong J.					
PA	(TULA-) TULARIX INC.					
PR	19-APR-1996; US-638237.					
PD	19-APR-1997.					
PN	WO97A0192-A1.					
FT	30-OCT-1997.					
FT	CDS					
OS	Homo sapiens.					
FH	Key					
FT	Location/Qualifiers					
FT	CD5					
FT	230..1798					
FT	/*tag= a					
KM	genetic disease; cell growth; cancer; inflammation;					
KW	nuclear factor kappa B; immune-regulated disease; infection;					
KW	hypersensitivity; diagnosis; therapy; ss.					
ID	T88990 standard; cDNA; 2248 BP.					
AC	T88990;					
DT	27-APR-1998 (first entry)					
DE	Tumour necrosis factor receptor associated factor 6 (TRAF6) cDNA.					
DE	Tumour necrosis factor receptor associated factor 6; TRAF6; human;					
CC	nuclear factor kappa B; immune-regulated disease; infection;					
CC	genetic disease; cell growth; cancer; inflammation;					
CC	hypersensitivity; diagnosis; therapy; ss.					
CC	DNA encoding tumour necrosis factor receptor associated factor 6 -					
CC	useful for screening compounds, for therapy and diagnosis of					
CC	immune-regulated diseases, etc.					
CC	Claim 4; Page 11-14; 23pp; English.					
CC	This cDNA sequence includes a coding region for a novel human					
CC	tumour necrosis factor receptor associated factor six (TRAF6)					
CC	polypeptide (see W32113), which transcriptionally activates nuclear					
CC	factor kappa-B. The 2248 bp sequence was isolated from human					
CC	spleen and umbilical vein endothelial cell cDNA libraries by					
CC	hybridisation with TRAF oligonucleotide probes. The isolated					
CC	nucleic acid is used to produce recombinant TRAF6. The recombinant					
CC	protein is used in a screening method for detecting agents that					
CC	modulate binding of TRAF6 to natural intracellular targets, while					
CC	cells containing the TRAF6 gene are used in a screening method for					
CC	detecting agents that modulate transcription of TRAF6-inducible					
CC	genes. Both methods are used to identify compounds potentially					
CC	useful in the diagnosis and treatment of immune-regulated diseases,					
CC	e.g. infection, genetic disease and disturbed cell growth/regulation					
CC	such as neoplasia, inflammation and hypersensitivity. Probes and					
CC	primers able to hybridise to the cDNA sequence are used to detect					
CC	TRAF6 mutations, to isolate natural TRAF6-encoding sequences, to					
CC	detect TRAF6 homologues and analogues, and therapeutically to					
CC	modulate cellular expression, or intracellular concentration of					
CC	TRAF6.					
CC	sequence					
CC	2248 BP;					
CC	635 A;					
CC	512 C;					
CC	515 G;					
CC	586 T;					
CC	TRAF6.					
CC	DNA encoding tumour necrosis factor receptor associated factor 6 -					
CC	useful for screening compounds, for therapy and diagnosis of					
CC	immune-regulated diseases, etc.					
CC	Claim 4; Page 11-14; 23pp; English.					
CC	This cDNA sequence includes a coding region for a novel human					
CC	tumour necrosis factor receptor associated factor six (TRAF6)					
CC	polypeptide (see W32113), which transcriptionally activates nuclear					
CC	factor kappa-B. The 2248 bp sequence was isolated from human					
CC	spleen and umbilical vein endothelial cell cDNA libraries by					
CC	hybridisation with TRAF oligonucleotide probes. The isolated					
CC	nucleic acid is used to produce recombinant TRAF6. The recombinant					
CC	protein is used in a screening method for detecting agents that					
CC	modulate binding of TRAF6 to natural intracellular targets, while					
CC	cells containing the TRAF6 gene are used in a screening method for					
CC	detecting agents that modulate transcription of TRAF6-inducible					
CC	genes. Both methods are used to identify compounds potentially					
CC	useful in the diagnosis and treatment of immune-regulated diseases,					
CC	e.g. infection, genetic disease and disturbed cell growth/regulation					
CC	such as neoplasia, inflammation and hypersensitivity. Probes and					
CC	primers able to hybridise to the cDNA sequence are used to detect					
CC	TRAF6 mutations, to isolate natural TRAF6-encoding sequences, to					
CC	detect TRAF6 homologues and analogues, and therapeutically to					
CC	modulate cellular expression, or intracellular concentration of					
CC	TRAF6.					

Query Match	2.68	Score 60.4	DB 1	Length 2248
Best Local Similarity	51.99	Pred. No. 1.4e-06		
Matches 164	Conservative	0	Mismatches 146	Indels 6
				Gaps
Oy	322	ggttacaagaagaaagcttctgttgaagaccgttggagagcaagtacaagatgttgaagatgccac	381a	
Db	392	GGATATGATGTAGTAGGTTTGACCCACCCTCGGAAGCAGATGTGTAATGCCCATCTGCTTG	451b	
Oy	382	ctgtgtctgttcagaccgccgaagcagaccgagtggtggagccgttcttcgagagctgcatg	441h	
Db	452	ATGGCATTTACAGAGAAGCAGTGCACCAACCCATGCGGCATAGTTCGTCCAAAGCCTGCATC	511i	
Oy	442	gcgcgccctgcgcgagctcttcacgtccaaatgttacaagcgtgtcaagaagacatcgttaa	501d	
Db	512	ATTTAAATCAATTAAGGAGTGCAGGTCACAAATGTCTCAATGTGACATGAAATATCTGTGAA	571j	
Oy	502	gataagtggtttaagagataatctgtctcaagagaganaattctgtgctcttcagatctatgt	561i	
Db	572	AATCAACATATTTCCAGACCAATTTTGCAAAACGTGACATCTTTCTCTGATGTGGAATGT	631k	
Oy	552	cygaatgtgaagcagaagtttggcgcagacagttaatgtcttggacatctcgtgcatttaaa	621n	
Db	632	CCAAATGA-----AGGTGTTTGCACAAAGATGGAACGTGACACTCTTGGAGATCATCAA	685B	
Oy	622	aatgatgtccattttg	637	
Db	686	GCACATTGTGAGTTTG	701	

RESULT 14
X28366/c
ID X28366 standard: DNA, 17425 BP.
AC X28366:
DT 18-JUN-1999 (first entry)
DE Human Stat6 gene.
KW Stat6; Statb; human; signal transducers and activators of transcription;
KW isoform; myeloid cancer; asthma; sarcoma; scleroderma; fibrotic disease;
KW bone marrow fibrosis; AIDS; Stat6c; ss.
OS Homo sapiens.
PN WC0910493-A1.
PD 04-MAR-1999.
PE 27-AUG-1998; U17821.
PR 05-JAN-1998; US-070397.
PR 27-AUG-1997; US-056075.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Larochele WJ, Patel B, Pierce JH;
DI WPI: 99-214517/18.
PT New isoforms of Stat6 - having differential effects on the
modulation of Stat6 activity in cells
PS Disclousure: Page 61-66: 88pp; English.
CC This sequence encodes human Stat6 (signal transducers and activators
of transcription). The invention relates to attenuated and dominant
negative isoforms of human Stat6. The detection and quantitation of DNA
or mRNA encoding Stat6 and/or Statb and/or Statc can be used to detect
differential expression of Stat6 isoforms in numerous diseases, including
myeloid cancer, asthma, sarcoma, scleroderma, bone marrow fibrosis,
fibrotic diseases and AIDS. The nucleic acids can be used to screen
genomic or cDNA libraries or to identify complementary sequences. The
identification of the genetic locus of the Stat6 gene can be used for
detection of chromosomal aberrations and translocations involving the
Stat6 gene. Antibodies against the isoforms can be used to detect the
presence of Stat6 and/or Statb and/or Statc in a sample. Because of the
variation of the roles of Statb and Statc in regulating gene
transcription the isolated and purified forms can be used to study gene
regulation and in screening assays for identifying drug candidates which
may be used as agonists or antagonists. The two polypeptides may also be
used in gene therapy protocols. In particular, Statb and/or Statc can
therapeutically modulate the development and differentiation of B and
T cells and can enhance IL-4 immunological function in immunocompromised
individuals. Stat6 activation correlates with functional responses
induced by interleukin-4 (IL-4), IL-13 and platelet-derived growth factor
(PDGF). Statb when compared Stat6 is an attenuated regulator of gene

CC transcription. Stat6c is a dominant negative regulator of gene
CC transcription.
SO Sequence 17425 BP; 3991 A; 4519 C; 4691 G; 4220 T;

Query Match

1.8%; Score 42.4; DB 1; Length 17425;
Best Local Similarity 60.3%; Pred. No. 0.35;

Matches 70; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 54 agatgaggaagaatgagcccaagaagtatgccacttggttaagtcaccagagcagtc 113
DB 121179 AGATGAGGAAGAATGAGCCCAAGAGTCGATGACTTGCCCGCTCATATGCTGCTA 12120
QY 114 agaatcagagccttagatcagaacacgtgctccgtcctgcctccctactctcta 169
DB 121119 AGAGGCGAGAGCTGAGATTAAACCCAGGCACTTGCGCCCTGAGACCCCTTAACCTA 12064

SULF 15

11319
AC V13119 standard; DNA; 1893 BP.

DE 11-JUN-1998 (first entry)
DE Synthetic B. thuringiensis truncated crystal protein 9C (cry9C) DNA.
KM Chimeric gene: plant cell transformation;
KM insecticidal crystal protein; ICP; cry9C;
KM AT-rich sequence expression; crystal protein 9C; ds.
OS Bacillus thuringiensis.
OS Synthetic.
FH Key
FH CDS
FT Location/Qualifiers
FT 9..1886
FT /*tag=8
FT /product= cry9C_(truncated)

PN WO9749814-A1.
PD 31-DEC-1997.
PF 30-MAY-1997; E02832.
PR 21-JUN-1996; US-667731.
PA (PLB2) PLANT GENETIC SYSTEMS NV.
PI Cornelissen M, Gosselle V, Meulewaeter F, Soetaert P,
PI Van Aartsen R;
DR WPI; 98-077117/07.
PT Chimeric gene providing high level expression of AT-rich sequences
PT in plants, useful for expressing insecticidal crystal proteins -
PT comprises promoter recognised by polymerase other than RNA
PT polymerase II which generates uncapped mRNA including two viral
PT translation enhancing sequences
PT Example 1; Pages 88-89; 108pp; English.
CC The present sequence was used in the preparation of a novel
CC chimeric gene, comprising: (a) promoter recognised by a
CC DNA-dependent RNA polymerase other than eukaryotic RNA polymerase
CC II; (b) DNA sequence encoding a chimeric RNA comprising 3' and 5'
CC untranslated regions (UTR), plus an AU-rich heterologous coding
CC sequence; and optionally (c) terminator recognised by the same
CC polymerase as the promoter. The chimeric RNA is uncapped,
CC translated in plant cell cytoplasm to form a protein and includes
CC two translation-enhancing sequences (TES) derived from the 5' and
CC 3' regions of (sub)genomic RNA of a positive stranded RNA plant
CC virus, located in corresponding 5' and 3' regions.
CC The chimeric gene can be used to transform plant cells which are
CC grown into plants that express the protein, specifically a Bacillus
CC thuringiensis insecticidal crystal protein (ICP), but more
CC generally any protein that improves, nutritional value, imparts
CC resistance to herbicides, pathogens or inhibits proteases,
CC amylases or RNases. TES provide efficient cap and polyadenylation
CC independent translation of RNA transcripts to give high protein
CC yields, while the use of a polymerase other than polymerase II
CC generates large amounts of uncapped/non-polyadenylated RNA, whereas
CC in current methods high yield expression of AT-rich genes is
CC difficult to achieve.
SO Sequence 1893 BP; 389 A; 681 C; 539 G; 284 T;

Query Match

1.8%; Score 41.4; DB 1; Length 1893;

Best Local Similarity 48.5%; Pred. No. 0.19;
Matches 114; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 1209 caagagatcggccctccgagacactggaggaagcagacagcatgaagcagcgt 1268
DB 323 CAACGCTGTAACAGCGCAGCCTCAGAACTGGCTGGCCGACCCCAACGACCCGCAACCT 382
QY 1269 ggaagtcctccagaaaccgagtgacagagctgagagcgctgagcaagagcggggaagt 1328
DB 383 GAGCGTGTGAGAGGCCCACTTCATCGCCCTGGAACCTGGAACCTGTAACGCAATCCCT 442
QY 1329 ggcctcgaaacacagagcctgtgagtcagcagcagcagcagcagcagcagcagcagc 1388
DB 443 GTTCGCGCTGAAACGCGCAGCAGAGTGCCTGCTGAGCGCTGTAACGCAACCTGTAACCT 502
QY 1389 gaagacatcagcagcctagccagacatgagacctggcctccagctcctgagacgcgc 1443
DB 503 GCACCTGCTGCTGTGAAGATGATCATCCCTGTTGCGCGAGGCGTGGGCTTCAC 557

Search completed: September 2, 2000, 09:52:03
Job time: 6182 sec

Sat Sep 2 10:45:16 2000

us-09-224-556-1.rng

Page 16


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Db 241 FQGTNOQIAHSSAVQVHNLKEMSNLEKRVSLQNESVEKKNISQSLHNOJCSFEI 300
QY 300 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKELDEIRPFROMWEADSMKSSVESLQNR 359
Db 301 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKELDEIRPFROMWEADSMKSSVESLQNR 360
QY 360 VTELESVDKSAQOVARNGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGLW 419
Db 361 VTELESVDKSAQOVARNGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGLW 420
QY 420 KIRDYRRRQOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGKGTHTLSLFFVIMRG 479
Db 421 KIRDYRRRQOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGKGTHTLSLFFVIMRG 480
QY 480 EYDALLPWFPOKQVTLMLMDQSSRRHLGDAFKPDNSSFFKPTGEMNIASGCPVFAQ 539
Db 481 EYDALLPWFPOKQVTLMLMDQSSRRHLGDAFKPDNSSFFKPTGEMNIASGCPVFAQ 540
QY 540 TVLENGTYIKDDTIFIKVIVDTSDLPDP 567
Db 541 TVLENGTYIKDDTIFIKVIVDTSDLPDP 568

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RESULT 2

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CD40 receptor-associated factor 1 - human
C:Species: Homo sapiens (man)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 10-Jul-1998
C:Accession: A55960
R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
Science 267, 1494-1498, 1995
A:Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
A:Reference number: A55960; MUID:95184010
A:Accession: A55960
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-568 <RES>
A:Cross-references: EMBL:U21092; NID:g726087; PID:g726088
C:Genetics:
A:Gene: CRAF1
C:Superfamily: RING finger homology
C:Keywords: zinc
F:49-97/Domain: RING finger homology <RNG>

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Query Match 99.2%; Score 2980.5; DB 2; Length 568;
Best Local Similarity 99.5%; Pred. No. 1e-164;
Matches 565; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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1 MESSKMDSPGALQTNPLKLTDRSAGTPVFPVPEGGYKKEKFKVTVEDKYCKECHLV 60
Db 1 MESSKMDSPGALQTNPLKLTDRSAGTPVFPVPEGGYKKEKFKVTVEDKYCKECHLV 60
QY 61 CSPKQTECHRCESCMALLSSSPKCTACQESIYKDKVFNCKCKREILALQIYCRNE 120
Db 61 CSPKQTECHRCESCMALLSSSPKCTACQESIYKDKVFNCKCKREILALQIYCRNE 120
QY 121 SRGCAEQLMLGH-LVHLKNDCHFEELPCVAPDCKEYLRKDLRDHYEKAACKYREATCSHC 179
Db 121 SRGCAEQLMLGH-LVHLKNDCHFEELPCVAPDCKEYLRKDLRDHYEKAACKYREATCSHC 180
QY 180 KQVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRLSELNHLSECVNAPSTCSFRKRGCV 239
Db 180 KQVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRLSELNHLSECVNAPSTCSFRKRGCV 240
QY 240 FQGTNOQIAHSSAVQVHNLKEMSNLEKRVSLQNESVEKKNISQSLHNOJCSFEI 299
Db 241 FQGTNOQIAHSSAVQVHNLKEMSNLEKRVSLQNESVEKKNISQSLHNOJCSFEI 300
QY 300 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKELDEIRPFROMWEADSMKSSVESLQNR 359
Db 301 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKELDEIRPFROMWEADSMKSSVESLQNR 360

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QY 360 VTELESVDKSAQOVARNGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGLW 419
Db 361 VTELESVDKSAQOVARNGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGLW 420
QY 420 KIRDYRRRQOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGKGTHTLSLFFVIMRG 479
Db 421 KIRDYRRRQOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGKGTHTLSLFFVIMRG 480
QY 480 EYDALLPWFPOKQVTLMLMDQSSRRHLGDAFKPDNSSFFKPTGEMNIASGCPVFAQ 539
Db 481 EYDALLPWFPOKQVTLMLMDQSSRRHLGDAFKPDNSSFFKPTGEMNIASGCPVFAQ 540
QY 540 TVLENGTYIKDDTIFIKVIVDTSDLPDP 567
Db 541 TVLENGTYIKDDTIFIKVIVDTSDLPDP 568

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RESULT 3

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CD40 receptor-associated factor 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Nov-1999
C:Accession: I49272
R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
Science 267, 1494-1498, 1995
A:Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
A:Reference number: A55960; MUID:95184010
A:Accession: I49272
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-567 <RES>
A:Cross-references: EMBL:U21050; NID:g719292; PIDN:AACS2175.1; PID:g719293
C:Genetics:
A:Gene: CRAF1
C:Superfamily: RING finger homology
C:Keywords: zinc finger
F:48-96/Domain: RING finger homology <RNG>

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Query Match 95.1%; Score 2859; DB 2; Length 567;
Best Local Similarity 95.6%; Pred. No. 1e-157;
Matches 543; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

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1 MESSKMDSPGALQTNPLKLTDRSAGTPVFPVPEGGYKKEKFKVTVEDKYCKECHLV 60
Db 1 MESSKMDAGTLQPPKLTQPDRAQS-VLVPDGGYKKEKFKVTVEDKYCKECHLV 59
QY 61 CSPKQTECHRCESCMALLSSSPKCTACQESIYKDKVFNCKCKREILALQIYCRNE 120
Db 60 CNPKQTECHRCESCMALLSSSPKCTACQESIYKDKVFNCKCKREILALQIYCRNE 119
QY 121 SRGCAEQLMLGH-LVHLKNDCHFEELPCVAPDCKEYLRKDLRDHYEKAACKYREATCSHC 179
Db 120 GRCGAELTLGLHLVHLKNDCHFEELPCVAPDCKEYLRKDLRDHYEKAACKYREATCSHC 179
QY 180 KQVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRLSELNHLSECVNAPSTCSFRKRGCV 239
Db 180 KQVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRLSELNHLSECVNAPSTCSFRKRGCV 239
QY 240 FQGTNOQIAHSSAVQVHNLKEMSNLEKRVSLQNESVEKKNISQSLHNOJCSFEI 299
Db 240 FQGTNOQIAHSSAVQVHNLKEMSNLEKRVSLQNESVEKKNISQSLHNOJCSFEI 299
QY 300 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKELDEIRPFROMWEADSMKSSVESLQNR 359
Db 300 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKELDEIRPFROMWEADSMKSSVESLQNR 359
QY 360 VTELESVDKSAQOVARNGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGLW 419
Db 360 VTELESVDKSAQOVARNGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGLW 419
QY 420 KIRDYRRRQOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGKGTHTLSLFFVIMRG 479
Db 420 KIRDYRRRQOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGKGTHTLSLFFVIMRG 479

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DB 420 KIRDYKRRKQZAVMGKTLISYQPFYTGFGKMCARVYLNDGKMGKTHLSLFYIMG 479
QY 480 EYDALLPMPFKOKVTLMDQSSRRHLDAKRPDPNSSFFKPTGEMNIASGCPVFAQ 539
DB 480 EYDALLPMPFKOKVTLMDQSSRRHLDAKRPDPNSSFFKPTGEMNIASGCPVFAQ 539
QY 540 TVLENGTYIKDDTIFIKVIVTSDLPD 567
DB 540 TVLENGTYIKDDTIFIKVIVTSDLPD 567

RESULT 4
568467
CD40 receptor-associated protein CAP-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C:Accession: S68467; I53498
R:Sato, T.; Irie, S.; Reed, J.C.
FEBS Lett. 358, 113-118, 1995
Title: A novel member of the TRAF family of putative signal transducing proteins binds
Reference number: I53498; MUID:95129692
A:Accession: S68467
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-543 <SAT>
A:Cross-references: EMBL:U38509; NID:9695357; PID:9695358
A:Experimental source: tissue-type fetal brain
C:Genetics:
A:Gene: CAP-1
C:Superfamily: RING finger homology
C:Keywords: homodimer; signal transduction; zinc; zinc finger
E:49-97/Domain: RING finger homology <RNG>

Query Match 93.6%; Score 2812; DB 2; Length 543;
Best Local Similarity 94.9%; Pred. No. 4.9e-155;
Matches 539; Conservative 0; Mismatches 3; Indels 26; Gaps 2;

QY 1 MSSSKMDSGALQTPRLKHTDRSAGTPVYVEGQYKKEKVKYVEDKYCKECHLV 60
DB 1 MSSSKMDSGALQTPRLKHTDRSAGTPVYVEGQYKKEKVKYVEDKYCKECHLV 60
QY 61 CSPKOTEGHRCFESCMALLSSSPKCTACOBSTYKDYVFNDCKRETLAQIYCRNE 120
DB 61 CSPKOTEGHRCFESCMALLSSSPKCTACOBSTYKDYVFNDCKRETLAQIYCRNE 120
QY 121 SSGCAEQMLAGH-LVHLKNDCHFEELPCVPRDCEKVKLRKDLRDHYEAKYREATCSHC 179
DB 121 SSGCAEQMLAGH-LVHLKNDCHFEELPCVPRDCEKVKLRKDLRDHYEAKYREATCSHC 180
QY 180 KQOVPMIALQKHEDDPCVVVSCPHKCSVQITLRSLSNAHSECVNADSTGCFKRYGCV 239
DB 181 KQOVPMIALQKHEDDPCVVVSCPHKCSVQITLRSLSNAHSECVNADSTGCFKRYGCV 217
QY 240 PGSTNOITAHSSAVOVHNLKEMNSLSEKVSLLQNSVEKNSISQSLHNOISFEL 299
DB 218 -GTNOITAHSSAVOVHNLKEMNSLSEKVSLLQNSVEKNSISQSLHNOISFEL 275
QY 300 ETEROKEMLRNNSKILHLQRYVDSQAEKLEKELRPFROMWEADSKSSVESLQNR 359
DB 276 ETEROKEMLRNNSKILHLQRYVDSQAEKLEKELRPFROMWEADSKSSVESLQNR 335
QY 360 VTELESVDKSAGOVANNTGILESQSLSRHDOMLSVHDIRLADMDLGFQVLETASNGVLW 419
DB 336 VTELESVDKSAGOVANNTGILESQSLSRHDOMLSVHDIRLADMDLGFQVLETASNGVLW 395
QY 420 KIRDYKRRKQZAVMGKTLISYQPFYTGFGKMCARVYLNDGKMGKTHLSLFYIMG 479
DB 396 KIRDYKRRKQZAVMGKTLISYQPFYTGFGKMCARVYLNDGKMGKTHLSLFYIMG 455
QY 480 EYDALLPMPFKOKVTLMDQSSRRHLDAKRPDPNSSFFKPTGEMNIASGCPVFAQ 539
DB 456 EYDALLPMPFKOKVTLMDQSSRRHLDAKRPDPNSSFFKPTGEMNIASGCPVFAQ 515

QY 540 TVLENGTYIKDDTIFIKVIVTSDLPD 567
DB 516 TVLENGTYIKDDTIFIKVIVTSDLPD 543

RESULT 5
J66539
tumor necrosis factor receptor-associated factor 5 homolog - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 17-Mar-1999
R:Mizushima, S.; Fujita, M.; Ishida, T.; Azuma, S.; Kato, K.; Hirai, M.; Otsuka, M.;
Gene 207, 135-140, 1998
A:Title: Cloning and characterization of a cDNA encoding the human homolog of tumor n
A:Reference number: J66539; MUID:98172745
C:Accession: J66539
A:Molecule type: mRNA
A:Residues: 1-557 <MT>
A:Cross-references: DDBJ:AB000509
C:Comment: This protein is involved in transduction of signals from various tumor nec
mphotoxin-beta receptor.
C:Genetics:
A:Map position: 1q32.3-1q41.1
C:Keywords: coiled coil; tumor; zinc finger

Query Match 39.3%; Score 1182; DB 2; Length 557;
Best Local Similarity 41.6%; Pred. No. 4.4e-61;
Matches 229; Conservative 121; Mismatches 181; Indels 20; Gaps 8;

QY 25 RSAGTPVYVEGQYKKEKVKYVEDKYCKECHLVLCSTKOTEGHRCFESCMALLS-S 83
DB 17 QNSGNSISLDFPESLEYOFERLEERYKCAFCHSVLHNPQTCGHRFCOHCILSLRELN 76
QY 84 SPSKACQESITVDFKVFNDCKRETLAQIYCRNESGCAEQMLAGHVLKNDCHFE 143
DB 77 TYPICPVNKEVILKSQEVFNDCCKREVLWLYYCSN-AGCAKAVILGKYODHLOQCLO 135
QY 144 ELPVPRDCEKVKLRKDLRDHYEAKYREATCSHCKSQVPMIALQKHEDDPCVVVSC 203
DB 136 PVQSNKRECPVLRKDLREHLASQCFRKEKLYCKKQVVVYINQNHENILCEPVPVC 195
QY 204 PHKCSVQITLRSLSNAHSECVNADSTGCFKRYGCVFQSTNOITAHSSAVOVHNLK 263
DB 196 PNNCA-KIILKTEVDENHLAVCEAEODCPFKHYGCAVTRKRRNLQHERSALREHRLV 254
QY 264 EMSNSLEKVSLLQNSVEKNSISQSLHNOISFELIEIEROKEMLRNNSKILHLQRYD 323
DB 255 EKNVQLEQISDLHLSLEQESKIQQLAETIKLEKEFKQFQLEKNSFLPNID-VERA 313
QY 324 SOAEKLEKELKEIRPE-----RQNWEEADSKSSVESLQNRTELESVDKSAGVARN 377
DB 314 SHIDKSAWLEAQVHQLQVNOQNKFDRLPLEANDVYKOKITLLEND-----QHL 366
QY 378 GLLESQSLRHDOMLSVHDIRLADMDLGFQVLETASNGVLIMKIRDYKRRKQZAVMGKTL 437
DB 367 AVLEETNKHHDHINIKHKAQLSKNEERFKLEGTGKNGKILIMKYVDYKKKKRAVAGHTV 426
QY 438 SLYSQPFYTGFGKMCARVYLNDGKMGKTHLSLFYIMRGYDALLPMPFKOKVTLMD 497
DB 427 SLFSQPFYTRSGYRLCAAYLNGDSSGSHSLSTLFVNRBEFDSLQMPFRQRYTLL 486
QY 498 MDQSSRRHLDAKRPDPNSSFFKPTGEMNIASGCPVFAQTVLEN--GTIYKDDTIF 555
DB 487 LQO-SGKKNIMETFKRPDPNSSFFKRPDGEEMNIASGCPRVAVSLVLEMANAYIKDDTIF 545
QY 556 KYIVTSDLPD 566
DB 546 KVAVDLTDLPD 556

RESULT 6

161512
 TNF receptor associated factor 2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: 161512
 R:Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
 Cell 78, 681-692, 1994
 A:Title: A novel family of putative signal transducers associated with the cytoplasmic d
 A:Reference number: A54750; MUID:94349371
 A:Accession: 161512
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-501 <RES>
 A:Cross-references: GB:I35303; NID:9532620; PIDN:AAC37662.1; PID:9532621
 C:Genetics:
 A:Gene: TRAF2
 C:Superfamily: RING finger homology
 C:Keywords: zinc
 F:30-78/Domain: RING finger homology <RNG>

Query Match

27.6%; Score 828; DB 2; Length 501;

Best Local Similarity 33.4%; Pred. No. 9, 9e-41;
 Matches 196; Conservative 90; Mismatches 190; Indels 110; Gaps 19;

QY 3 SSKKMDSPGALQTNPIKHTDSAGTFFVPPGQYKEKFKVT-VEDKYKCEKHLVLC 61
 Db 2 AASVTSFGSLLELP-----GFSKTLGTRLKAKYLCSACKNRLR 42
 QY 62 SPQTEGCHPFCSCMAALLSSSPKCTAC-----QESI---VKDFKDNCKREILA 112
 Db 43 RPPQACGHRGSCFCLASISGPGONCAACYEBGLYEGISLESSAFDNARRVES 102
 QY 113 LQIYCRNESGCAEQMLGHLVHLKNDCHFEELPCVR---PDCEKYLKDLNDHYEKAC 169
 Db 103 LPAPCPMD--GCTWK---GTLKEYES-CHGELCPFLTECPACKGLVRLSEKEHTEQEC 156
 QY 170 KYRPAATGSHCKSQVPMALAKHEPTDPCVAVSGPHKCSQVTLRLSLHLSHCVNAPS 229
 Db 157 PKRSLSCOHCRAPCSHVDLEHYEV-CPKRPPLTC-DGCGKKKIPRETFFQDHVRACSKCY 214
 QY 230 TCSKRRGCVFQGTNOQIKAHESAVOHVNLKEMNSLEKVS-----LLQNE 279
 Db 215 LCRHYVGCSEMTVENLOHDLRLKRLALL--LSFLEAQSPTLQVGEELLQRC 272
 QY 280 SVEKNKSIQSLHNOISFEIEIEROKEMLRNNEKIIHLQVYDSQAEKLEKDETRPF 339
 Db 273 QILBOK-IAPFENIVCVLNEVER-----VAVTAEACSRQHRLDOD--- 312
 QY 340 RQNNEDSMKSSVESLQNRVTELESVDKSAQVARNRTGLESQLSRHQDLVSHDIRLA 399
 Db 313 -----KTEALSNKVOOLE-----RSIGL-----KDLAMA 336
 QY 400 DMDLGQVLEIETASYNGVLIWKIRDYKRRKQEAAGKTLSTYSQFYTGFGYKMCARYTL 459
 Db 337 DLDEKVSLEIETASYNGVLIWKIRDYKRRKQEAAGKTLSTYSQFYTGFGYKMCARYTL 396
 QY 460 NGDGKGTHTLSLFFVYMRGEYDALLPPEFQOKYTLMLMDQSSRRHLDGAFKRDPPSS 519
 Db 397 NGDPTGRGTHLSLFFVYMRGEYDALLPPEFQOKYTLMLMDH-NNRREHIDAFRDVTS 455
 QY 520 FKRPTEGNIAAGCVFAQVLE-NGYIKQDTFIFIKVYDTSDL 564
 Db 456 FQRPVSDMNIAAGCVFAQVLE-NGYIKQDTFIFIKVYDTSDL 501

RESULT 7

S56163

tumor necrosis factor receptor-associated protein - human
 N:Alternate names: TNF receptor-associated protein
 C:Species: Homo sapiens (man)
 C:Date: 10-Oct-1995 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999
 C:Accession: S56163; S58925; S58926

R:Song, H.Y.; Donner, D.B.
 Biochem. J. 309, 825-829, 1995
 A:Title: Association of a RING finger protein with the cytoplasmic domain of the huma
 A:Reference number: S56163; MUID:95366958
 A:Accession: S56163
 A:Molecule type: mRNA
 A:Residues: 1-501 <SON>
 A:Cross-references: EMBL:U12597
 R:Song, H.Y.; Donner, D.
 submitted to the EMBL Data Library, July 1994
 A:Description: Association of a RING finger protein with the cytoplasmic domain of th
 A:Reference number: S58925
 A:Accession: S58925
 A:Molecule type: mRNA
 A:Residues: 1-42, 63-342, 363-501 <SOW>
 A:Cross-references: EMBL:U12597
 A:Accession: S58926
 A:Molecule type: mRNA
 A:Residues: 1-342, RPPQACGHRGSCFCLASIL, 363-501 <SOF>
 A:Cross-references: EMBL:U12597; NID:975272; PIDN:AAAB7706.1; PID:975273
 C:Superfamily: RING finger homology
 C:Keywords: zinc finger
 F:30-78/Domain: RING finger homology <RNG>

Query Match

26.7%; Score 802.5; DB 2; Length 501;

Best Local Similarity 35.3%; Pred. No. 2, 9e-39;
 Matches 196; Conservative 87; Mismatches 176; Indels 97; Gaps 22;

QY 36 QGGYKEKFKVT-VEDKYKCEKHLVLCSPKQTEGCHPFCSCMAALLSSSPKCTAC-OE 93
 Db 16 QGFSKTLGTRLKAKYLCSACKNRLRPPQACGHRGSCFCLASISGPGONCAACYHE 75
 QY 94 SYKDKV-----FKDNCKREILAQIYCRNRSRGCAEQMLGHLVHLKNDCHFEEL 145
 Db 76 GYIEEGISLESSAFPDNARRVESLPAVC--PSDGTWK---GTLKEYES-CHGRC 129
 QY 146 PCVR---PDCEKYLKDLNDHYEKACRYEATCSHCKSQVPMALOKHEDIDPCVAVS 202
 Db 130 PLMLTGPCRACKGLVRLSEKEHRLHEHCPERSLSCHRCRAPCGADVKAHVEY-CPKPLT 188
 QY 203 CPKCSQVQTLNSELSEAHLSQCVNAPSTCSFKRYCV--FQGTNOQIRAHESAVOHVN 260
 Db 189 C-DGCGKKKIPREKFDHVKTCGRVPCFRFALICGLEVEGEKQO--EHEVQMLREHLA 245
 QY 261 LKEMNSLEK-----VSILQN-ESEYKNSISQSLNOICSEFIEIEROKEMLR 309
 Db 246 ML--LSVLEAKPLGCDQSHAGSELLQRCSELEKTA--TFENIVCVLNEVER----- 295
 QY 310 NNEKSIHLQVYDSQAEKLEKDEIRPFRQNNEDSMKSSVESLQNRVTELESVDKS 369
 Db 296 -----VAVTAEACSR-----RQHRLDOD-----KTEALSNKVOOLE----- 325
 QY 370 AGOVARNRTGLESQLSRHQDLVSHDIRLADMDLGQVLEIETASYNGVLIWKIRDYKRRKQ 429
 Db 326 -----RSIGL-----KDLAMADLEQVLEIETASYNGVLIWKIRDYKRRKQ 366
 QY 430 EAVMGKTLISQPFYTGFGYKMCARYTLNGDGMRGTHLSLFFVYMRGEYDALLPPEF 489
 Db 367 EAVAGRPALFPAFTTSRGTGRCRLITLNDGCRGTHLSLFFVYMRGEYDALLPPEF 426
 QY 490 KQVYTLMLMDQSSRRHLDGAFKRDPPNSSFKKPTEGNIAAGCVFAQVLE-NGYIK 548
 Db 427 NQVYTLMLMDQ-NNRREHIDAFRDVTSFQRPVSDMNIAAGCVFAQVLE-NGYIK 485
 QY 549 KQDTIFIKVYDTSDL 564
 Db 486 RDDAIFIKVYDTSDL 501

RESULT 8

I38729

tumor necrosis factor type 2 receptor associated protein 3 - human

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 2, 2000, 10:21:48 ; Search time 38.17 Seconds

(without alignments)
460.331 Million cell updates/sec

Title: US-09-224-556-2

Perfect score: 3005

Sequence: 1 MESSKRMDSFALQTNPLK.....IKDDTIFIKYVDTSLPP 567

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Minimum number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2980.5	99.2	568	1	TRA3_HUMAN
2	2859	95.1	567	1	TRA3_MOUSE
3	828	27.6	501	1	TRA2_MOUSE
4	735.5	24.5	501	1	TRA2_HUMAN
5	637.5	21.2	416	1	TRA1_HUMAN
6	629	20.9	409	1	TRA1_MOUSE
7	189.5	6.3	458	1	DG17_DICDI
8	151.5	5.0	704	1	MEPB_MOUSE
9	145	4.8	1104	1	NFX1_HUMAN
10	140.5	4.7	624	1	A33_PLENA
11	140	4.7	1102	1	MISC_CHICK
12	140	4.7	3210	1	CENF_HUMAN
13	138.5	4.6	1957	1	YD86_SCHPO
14	136	4.5	704	1	MEPB_RAT
15	135	4.5	1607	1	MIPR_YEAST
16	133	4.4	944	1	NUP1_YEAST
17	132.5	4.4	389	1	ENAM_BOVIN
18	132	4.4	1940	1	MISE_RAT
19	131.5	4.4	724	1	HMR_HUMAN
20	131.5	4.4	1679	1	Y109_YEAST
21	131	4.4	1940	1	MYSE_HUMAN
22	130.5	4.3	1928	1	MYSL_YEAST
23	130	4.3	1106	1	STC_DROME
24	130	4.3	1940	1	MISE_CHICK
25	129.5	4.3	1225	1	SMC1_YEAST
26	129	4.3	700	1	MEPB_HUMAN
27	129	4.3	1816	1	LMA4_HUMAN
28	128.5	4.3	285	1	TPM1_DROME
29	128.5	4.3	504	1	TPM5_DROME
30	128.5	4.3	518	1	TPM4_DROME
31	127	4.2	1290	1	XCP4_XENLA
32	127	4.2	1939	1	MYSA_HUMAN
33	126.5	4.2	283	1	TPMM_LOCMT

34	126	4.2	252	1	TPM3_DROME	P09492 drosophila
35	126	4.2	747	1	MEPB_MOUSE	P28825 mus musculu
36	125	4.2	794	1	HMR_MOUSE	P00547 mus musculu
37	125	4.2	1073	1	RAG1_ONCMY	P09187 oncorhynchu
38	125	4.2	1084	1	MYSS_RABIT	P02562 oncotolagus
39	125	4.2	1863	1	BRCL_HUMAN	P38398 homo sapien
40	125	4.2	2663	1	CENF_HUMAN	P02224 homo sapien
41	124.5	4.1	1935	1	MYSB_RAT	P02564 rattus norv
42	124	4.1	748	1	MYSA_RAT	P064230 rattus norv
43	124	4.1	1039	1	YAF3_SCHPO	P09857 schizosach
44	123.5	4.1	783	1	ZFY2_MOUSE	P20662 mus musculu
45	123.5	4.1	876	1	MYSS_HUMAN	P12882 homo sapien

ALIGNMENTS

RESULT ID	TRA3_HUMAN	STANDARD	PRT	568 AA.
AC	Q1314: Q13076; Q13947; Q12990;			
DT	15-FEB-2000 (Rel. 39, Created)			
DT	15-FEB-2000 (Rel. 39, Last sequence update)			
DT	15-FEB-2000 (Rel. 39, Last annotation update)			
DE	TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)			
DE	(CRAFT) (CD40 BINDING PROTEIN) (CD40BP) (LMP1 ASSOCIATED PROTEIN)			
DE	(LAP1)			
GN	TRA3 OR CRAFT OR CAP-1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 95184010.			
RA	Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;			
RT	"Involvement of CRAFT, a relative of TRAF, in CD40 signaling."			
RL	Science 267:1494-1498(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISSUE-LYMPHOMA;			
RX	MEDLINE: 95163092.			
RA	Mosialos G., Birkendach M., Yalamanchili R., Vandersdale T., Ware C.;			
RT	Kieff E.;			
RL	"The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family."			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-FETAL BRAIN;			
RX	MEDLINE: 95129692.			
RA	Sato T., Irie S., Reed J.C.;			
RT	"A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40."			
RL	FEBS Lett. 358:113-118(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE: 95073988.			
RA	Hu H.M., O'Rourke K., Boguski M.S., Dixit V.M.;			
RT	"A novel RING finger protein interacts with the cytoplasmic domain of CD40."			
RL	J. Biol. Chem. 269:30069-30072(1994).			
CC	- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.			
CC	- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR ASSOCIATED FACTORS (POTENTIAL).			
CC	- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.			
CC	- SIMILARITY: CONTAINS A MATH/TRAFF DOMAIN.			
CC	THIS SWISS-PROT ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY			


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OY 121 SRGAEOLMLGH-LVHLKNDCHFEELPCVPRDCKEVLKRDLDHYEKACKYREATCSHC 179
DB 120 GRCGEOLTLGLVHLKNECOFEEPCRADCKEVLKRDLDHYEKACKYREATCSHC 179
OY 180 KSOVMIALQKHEDTDCPCVVSCHPKSCVQTLRLSELSEHLSECVNAPSTCSFRKGYC 239
DB 180 KSOVMIALQKHEDTDCPCVVSCHPKSCVQTLRLSELSEHLSECVNAPSTCSFRKGYC 239
OY 240 FQGTNOQIKAHBASSAVQVHNLKEMNSLEKRVSLQNESEYKKNKSIGSLNNOICSEI 299
DB 240 FQGTNOQIKAHBASSAVQVHNLKEMNSLEKRVSLQNESEYKKNKSIGSLNNOICSEI 299
OY 300 EIEREKEMRNNESTKILHQRVIDSOAEKLEKLEIRFRONWEADSKSSVESLQNR 359
DB 300 EIEREKEMRNNESTKILHQRVIDSOAEKLEKLEIRFRONWEADSKSSVESLQNR 359
OY 360 VTELESVDKASGOVANTGLLESQSLSRHDOMLSVHDIRLADMDLGFQVETASYNGVLIM 419
DB 360 VTELESVDKASGOVANTGLLESQSLSRHDOMLSVHDIRLADMDLGFQVETASYNGVLIM 419
OY 420 KIRDYKRRKQEAVMGKTSLSYQPFYTGFGYKMCARYLNGDMGKGTLSLFEVIMRG 479
DB 420 KIRDYKRRKQEAVMGKTSLSYQPFYTGFGYKMCARYLNGDMGKGTLSLFEVIMRG 479
OY 480 EVDALLPWFKRVKVTLMMDQSSRRHLGDAKRPDPNSSFFKPGEMNIAAGCPYFAQ 539
DB 480 EVDALLPWFKRVKVTLMMDQSSRRHLGDAKRPDPNSSFFKPGEMNIAAGCPYFAQ 539
OY 540 TVLENGTYIKDITFIKVIYVTSDDLDP 567
DB 540 TVLENGTYIKDITFIKVIYVTSDDLDP 567

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RESULT 3

```

ID TRAF2_MOUSE STANDARD: PRT: 501 AA.
AC P39429:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2).
GN TRAF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
MEDLINE: 94349371.
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.:
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
CC ACTIVATES NF-KAPPA-B.
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
CC HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
CC PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS
CC FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC -1- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL, L35303; AAC37662.1;

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DR MGD: MGI:101835; TRAF2.
DR PFAM: PF000917; MATH: 1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4_1.
DR ZINC_FINGER: Coiled coil.
FT 2N_FING 34 72 C3HC4-TYPE.
FT DOMAIN 298 348 COILED COIL (POTENTIAL).
FT DOMAIN 334 501 MATH/TRAF.
SQ SEQUENCE 501 AA: 56026 MW: 043B391180365F10 CAC64;

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Query Match 27.6%; Score 828; DB 1; Length 501;
 Best Local Similarity 33.4%; Pred. No. 4.2e-43;
 Matches 196; Conservative 90; Mismatches 190; Indels 110; Gaps 19;

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OY 3 SSKKSDSPGALQTNPLKLTHTDSAGTPVPEQGYKEKFEVKT-VEDKYKCEKHLVLC 61
DB 2 AAASYTSPGSLTLQP-----GFSKTLIGTLRLAKYLCSSACKNLR 42
OY 62 SPKQTECGHRCFESCMALSSSPKCTAC-----QESI---VADKYKNDCKREILA 112
DB 43 RPFQACGCHRYCSFGLTSLSSGPONCAQVYEGLYEEGISLESSAFPDMAAREVBS 102
OY 113 IQIYCRNBSRGCAEOLMLGLVHLKNDCHFEELPCVR--PPCKEVLKRDLDHYEKAC 169
DB 103 LPVAVPND--GCTWK---GTLKEYES-CHGGLCPFLITCPCPKGLVRLSEKHEHTDEC 156
OY 170 KYREATSCCHKQVVMIALQKHEDTDCPCVVSCHPKSCVQTLRLSELSEHLSECVNAPS 229
DB 157 PKRSLSCGKRAPCSHVLDVHEV-CRKFPLTC-DGCGKKIIPRETFQDHRACSKAV 214
OY 230 TCSFKRYGCVFQGTNOQIKAHBASSAVQVHNLKEMNSLEKRV-----LLONE 279
DB 215 LCRFHTVGCSEWVETENLQDHELQRLREHLAL--LSFLFAQASGTLNOVGPELQRC 272
OY 280 SYEKNSIQSLNNOICSEIFEIEREKEMRNNESTKILHQRVIDSOAEKLEKLEIRFP 339
DB 273 QLEBOK-TAFENIYCVLNEVER-----VAATACSKQHRLLDQ--- 312
OY 340 RONWEADSKSSVESLQNRVTELESVDKASGOVANTGLLESQSLSRHDOMLSVHDIRLA 399
DB 313 -----KIEALSINKVOGLE-----RSISL-----KOLAVA 336
OY 400 DMDLGFQVLETASYNGVLIMKIRDYKRRKQEAVMGKTSLSYQPFYTGFGYKMCARYL 459
DB 337 DLEQKVSLEVTYDGVFVWKISDFTKROEAVAGTPAIFSPATYTSYRGKMCRLRYL 396
OY 460 NGDGMGKGTLSLFEVIMRGVYDALLPWFKRVKVTLMMDQSSRRHLGDAKRPDPNSS 519
DB 397 NQDGGRGKGTLSLFEVIMRGVYDALLPWFKRVKVTLMMDQSSRRHLGDAKRPDPNSS 455
OY 520 FKRPTEGNINAGCPYFAQVYLE-NGTYIKDITFIKVIYVTSDDL 564
DB 456 FQRPVSDMNINAGCPYFAQVYLE-NGTYIKDITFIKVIYVTSDDL 501

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RESULT 4

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ID TRAF2_HUMAN STANDARD: PRT: 501 AA.
AC Q12933:
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2) (TUMOR NECROSIS FACTOR TYPE 2
DE RECEPTOR ASSOCIATED PROTEIN 3).
GN TRAF2 OR TRAF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RX SEQUENCE FROM N.A.
MEDLINE: 95366958.
RA Song H.Y., Donner D.B.;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 2, 2000, 10:20:59 ; Search time 54.15 Seconds
(without alignments)
725.992 Million cell updates/sec

Title: US-09-224-556-2
Perfect score: 3005
Sequence: 1 MESSKMDSPGALQTNPLK.....IKDDTIFIKVIVTSDLPDP 567

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Matched: 225878 seqs, 69334122 residues
Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-REMBL_12:*
2: sp-archaea:*
3: sp-bacteria:*
4: sp-fungi:*
5: sp-human:*
6: sp-invertebrate:*
7: sp-mammal:*
8: sp-mhc:*
9: sp-organelle:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2980.5	99.2	568	4	Q13114
2	2859	95.1	567	4	Q60803
3	1244	41.4	558	11	P70191
4	1244	41.4	558	11	Q61480
5	1182	39.3	557	4	O00463
6	822.5	27.4	508	11	O54896
7	735.5	24.5	501	4	Q12933
8	637.5	21.2	416	4	Q13077
9	554.5	18.5	522	4	Q9Y4K3
10	534	18.4	470	4	Q14848
11	537.5	17.9	530	11	P70196
12	520	17.3	470	11	Q61382
13	519	17.3	509	5	O62248
14	506.5	16.9	486	5	O9YXR0
15	260.5	8.7	463	5	O9YXQ9
16	208	6.9	198	4	O75615
17	169	5.6	528	13	Q91885
18	164	5.5	891	4	O9Y2K3
19	159	5.3	852	2	O9X1X1

20	156.5	5.2	808	4	O15083	O15083 homo sapien
21	156	5.2	1816	11	O88785	O88785 mus musculu
22	152	5.1	1816	11	P97927	P97927 mus musculu
23	151.5	5.0	634	11	O61510	O61510 mus musculu
24	150.5	5.0	1676	10	O23332	O23332 arabidopsis
25	149	5.0	919	1	O9YFZ1	O9YFZ1 aeropyrum p
26	147.5	4.9	1005	1	O58718	O58718 methanococ
27	147	4.9	609	13	O92021	O92021 xenopus lae
28	146.5	4.9	610	13	O91431	O91431 xenopus lae
29	145	4.8	713	13	O9YHD6	O9YHD6 rana catesb
30	145	4.8	1300	4	O13999	O13999 homo sapien
31	144.5	4.8	846	4	O75130	O75130 homo sapien
32	144	4.8	1364	13	O90631	O90631 gallus gall
33	143	4.8	1577	5	O20795	O20795 caenorhabd
34	142.5	4.7	476	13	O91940	O91940 xiphophorus
35	142.5	4.7	2253	13	P70012	P70012 xenopus lae
36	142	4.7	412	5	O16684	O16684 caenorhabd
37	142	4.7	1356	4	O14707	O14707 homo sapien
38	142	4.7	1583	4	O15045	O15045 homo sapien
39	141	4.7	2230	4	O13439	O13439 homo sapien
40	140	4.7	879	1	O58687	O58687 pyrococcus
41	139.5	4.6	3113	4	O13246	O13246 homo sapien
42	139	4.6	1012	4	O75665	O75665 homo sapien
43	139	4.6	1218	11	O70365	O70365 mus musculu
44	138	4.6	1690	5	O44929	O44929 drosophila
45	137.5	4.6	1974	5	O21000	O21000 caenorhabd

ALIGNMENTS

RESULT 1

ID Q13114 PRELIMINARY; PRT; 568 AA.

AC Q13114; Q13076; Q13947; Q12990;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1) (CRF3) (LMP1 ASSOCIATED PROTEIN) (LAP1).

GN TNF3 OR CRF1 OR CAP-1 OR CD40BP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95184010.

RA CHENG G., CLEARY A.M., YE Z.S., HONG D.I., LEDERMAN S., BALTIMORE D., "Involvement of CRF1, a relative of TRAF, in CD40 signaling.", Science 267:1494-1498(1995).

RL [2]

RP SEQUENCE FROM H.A., AND CHARACTERIZATION.

RC TISSUE-LYMPHOMA;

RX MEDLINE; 95163092.

RA MOSTALOS G., BIRKENBACH M., YALAMANCHILI R., VANARSDALE T., WARE C., KIERF E., "The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family.", Cell 80:389-399(1995).

RL [3]

RP SEQUENCE FROM N.A.

RC TISSUE-PERIL BRAIN;

RX MEDLINE; 95129692.

RA SATO T., IRIE S., REED J.C., "A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40.", FEBS Lett. 358:113-118(1995).

RL [4]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95073988.

RA HU H.M., O'ROURKE K., BOGUSKI M.S., DIXIT V.M., "A novel RING finger protein interacts with the cytoplasmic domain of CD40.",

RL J. Biol. Chem. 269:30069-30072(1994).
 CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
 CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.
 CC -1- FUNCTION: MAY BE INVOLVED IN GASTRULATION (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
 CC ASSOCIATED FACTORS (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 DR EMBL: U21092; AAC5012.1; -
 DR EMBL: U19260; AAA65732.1; -
 DR EMBL: U138509; AAA68195.1; -
 DR EMBL: U15637; AAA56753.1; -
 DR MIM: 601896; -
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 DR PFAM: PF00917; MATCH; 1.
 DR PFAM: PF00097; zf-C3HC4; 1.
 KW Zinc-finger; Coiled coil.
 FT ZN_FING 68 77 C3HC4-TYPE.
 FT DOMAIN 267 338 COILED COIL (POTENTIAL).
 FT CONFLICT 129 129 T -> M (IN REF. 2 AND 4).
 FT CONFLICT 134 134 MISSING (IN REF. 4).
 FT CONFLICT 218 242 MISSING (IN REF. 3).
 FT CONFLICT 339 339 P -> S (IN REF. 3).
 FT CONFLICT 405 405 R -> G (IN REF. 4).
 SQ SEQUENCE 568 AA; 64459 MW; 77A8CBDB CRC32;

Query Match 99.2%; Score 2980.5; DB 4; Length 568;
 Best Local Similarity 99.5%; Pred. No. 2,3e-181;
 Matches 565; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVFEDEGGYKEKFKYEDKCKCHLV 60
 DB 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVFEDEGGYKEKFKYEDKCKCHLV 60
 QY 61 CSPRQTEGHRFCSCMAALLSSSPCTACQESIVADKYKDCCKREILALQYCRNE 120
 DB 61 CSPRQTEGHRFCSCMAALLSSSPCTACQESIVADKYKDCCKREILALQYCRNE 120
 QY 121 SRGCAEOLMIGH-LVHKNDCHEFEELPCVRPDECKEYLRKDLRDHVEKACKYREATCSHC 179
 DB 121 SRGCAEOLMIGH-LVHKNDCHEFEELPCVRPDECKEYLRKDLRDHVEKACKYREATCSHC 180
 QY 180 KSGVPMIALOKHEDTDCPCVVVSCPHKCSVOTLLRSELSAHLSVCVNA PSTCSFKRYGCV 239
 DB 181 KSGVPMIALOKHEDTDCPCVVVSCPHKCSVOTLLRSELSAHLSVCVNA PSTCSFKRYGCV 240
 QY 240 FQGTNOQIKAEASAVOHVLLKEMSNLEKYSILQNESVEKNKSIQSLAHQICSEI 299
 DB 241 FQGTNOQIKAEASAVOHVLLKEMSNLEKYSILQNESVEKNKSIQSLAHQICSEI 300
 QY 300 EIERQKMLRNNESEKILHLQVIDSOAEKLELDKEIRPFQNMEEADSMKSVSIESLQNR 359
 DB 301 EIERQKMLRNNESEKILHLQVIDSOAEKLELDKEIRPFQNMEEADSMKSVSIESLQNR 360
 QY 360 VTELESYDKSAGVARTGLLESQLSRHDQMLSYHDIRLAMDYGFQVLETAASNGVLIW 419
 DB 361 VTELESYDKSAGVARTGLLESQLSRHDQMLSYHDIRLAMDYGFQVLETAASNGVLIW 420
 QY 420 KIRYKRRKQAVVNGKTLSTYSOPFYGYEYKMKCARVYLLGDDGKGTSLSTLFFVIRG 479
 DB 421 KIRYKRRKQAVVNGKTLSTYSOPFYGYEYKMKCARVYLLGDDGKGTSLSTLFFVIRG 480
 QY 480 EYDALLPMPFKOKYTIMLMDQSSRRHLGDAFKPDNNSSEFKKPTGENNIAAGCPVFAQ 539
 DB 481 EYDALLPMPFKOKYTIMLMDQSSRRHLGDAFKPDNNSSEFKKPTGENNIAAGCPVFAQ 540
 QY 540 TVLENGYIKDDTIFIKYIVDTSLPDP 567
 DB 541 TVLENGYIKDDTIFIKYIVDTSLPDP 568

RESULT 2

060803
 ID 060803 PRELIMINARY; PRT: 567 AA.
 AC 060803; 062380;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)
 DE (CRAFT) (TRAFFAMN).
 GN TRAF3 OR CRAFT OR TRAFAMN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95184010.
 RA CHENG G., CLEARY A.M., YE Z., HONG D.I., LEDERMAN S., BALTIMORE D.;
 RT "Involvement of CRAFT, a relative of TRAF, in CD40 signaling.";
 RL Science 267:1494-1498(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN-C57BL/6J; TISSUE-BRAIN;
 RX MEDLINE: 96299439.
 RA WANG X., BORNISLAEGER E.A., HAUB O., TOMIHARA-NEUBERGER C., LONBERG N.,
 RA DINILOS M.B., DISTECHE C.M., COPELAND N., GILBERT D.J., JENKINS N.A.,
 RA LACY E.;
 RT "A candidate gene for the amniotless gastrulation stage mouse mutation
 RT encodes a TRAF-related protein.";
 RL Dev. Biol. 177:274-290(1996).
 CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
 CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR (BY SIMILARITY).
 CC -1- FUNCTION: MAY BE INVOLVED IN GASTRULATION.
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
 CC ASSOCIATED FACTORS (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN
 CC KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT
 CC FOUND IN LIVER.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST
 CC LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION,
 CC FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
 CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 DR EMBL: U21050; AAC52175.1; -
 DR EMBL: U33840; AAC52710.1; -
 DR MGD: MGI:108041; Traf3.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 DR PFAM: PF00917; MATCH; 1.
 DR PFAM: PF00097; zf-C3HC4; 1.
 KW Zinc-finger; Coiled coil.
 FT ZN_FING 67 76 C3HC4-TYPE.
 FT DOMAIN 266 337 COILED COIL (POTENTIAL).
 FT CONFLICT 72 73 CE -> WQ (IN REF. 2).
 FT CONFLICT 390 390 T -> M (IN REF. 2).
 SQ SEQUENCE 567 AA; 64263 MW; F85A30F3 CRC32;

Query Match 95.1%; Score 2859; DB 11; Length 567;
 Best Local Similarity 95.6%; Pred. No. 1.1e-173;
 Matches 545; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVFEDEGGYKEKFKYEDKCKCHLV 60
 DB 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVFEDEGGYKEKFKYEDKCKCHLV 59
 QY 61 CSPRQTEGHRFCSCMAALLSSSPCTACQESIVADKYKDCCKREILALQYCRNE 120
 DB 60 CSPRQTEGHRFCSCMAALLSSSPCTACQESIVADKYKDCCKREILALQYCRNE 119
 QY 121 SRGCAEOLMIGH-LVHKNDCHEFEELPCVRPDECKEYLRKDLRDHVEKACKYREATCSHC 179
 DB 120 SRGCAEOLMIGH-LVHKNDCHEFEELPCVRPDECKEYLRKDLRDHVEKACKYREATCSHC 179
 QY 180 KSGVPMIALOKHEDTDCPCVVVSCPHKCSVOTLLRSELSAHLSVCVNA PSTCSFKRYGCV 239
 DB 180 KSGVPMIALOKHEDTDCPCVVVSCPHKCSVOTLLRSELSAHLSVCVNA PSTCSFKRYGCV 239

Db 180 KSGVPMIKLKHEDTDCPVVSCPHKCSVOTLLRSELSEAHLSVCVNAFSTCSFRRYGCV 239
QY 240 FQGINQOIKAHKHAESSAVQHVWMLKEMNSLSLEKKSLLQNESEVENKKSIOSLHNOICSEI 299
Db 240 FQGINQOIKAHKHAESSAVQHVWMLKEMNSLSLEKKSLLQNESEVENKKSIOSLHNOICSEI 299
QY 300 EIEHOKEMLRNNEKSIHLQVIDSQAELKELDKETIRPFQONWEADSMKSSESLONR 359
Db 300 EIEHOKEMLRNNEKSIHLQVIDSQAELKELDKETIRPFQONWEADSMKSSESLONR 359
QY 360 VTELESVDKSGQVARTGLLESQLSRHDOMLSYHDIRLADMGLFOYLETASNGVLIW 419
Db 360 VTELESVDKSGQVARTGLLESQLSRHDOMLSYHDIRLADMGLFOYLETASNGVLIW 419
QY 420 KIRYKRRKQAVNGKTLSTLSOPEFTYGFYKMCARYLNGDMGKTHLSLFFVIMRG 479
Db 420 KIRYKRRKQAVNGKTLSTLSOPEFTYGFYKMCARYLNGDMGKTHLSLFFVIMRG 479
QY 480 EYDALLPMPFKOKYTLMLMDGSSRRHLGDAFKPDPNSSFKPTGEMNINSGCPVFAQ 539
Db 480 EYDALLPMPFKOKYTLMLMDGSSRRHLGDAFKPDPNSSFKPTGEMNINSGCPVFAQ 539
QY 540 TVLENGTYIKDITFIKVIYDTSIDLPD 567
Db 540 TVLENGTYIKDITFIKVIYDTSIDLPD 567

RESULT 3
ID P70191 PRELIMINARY; PRT; 558 AA.
AC P70191;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TRAF5.
GN TRAF5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96382484.
RA ISHIDA T., TOJO T., AOKI T., KOBAYASHI N., OHISHI T., WATANABE T.,
RY YAMAMOTO T., INOUE J.;
RT "TRAF5, a novel tumor necrosis factor receptor-associated factor
family protein, mediates CD40 signaling.";
Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).
-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL: D83528; BA11942.1; -
MGI: 107548; Traf5.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
DR PFM: PFO0917; MATH; 1.
DR PFM: PFO0097; Zf-C3HC4; 1.
KM Zinc-finger.
SQ SEQUENCE 558 AA; 64145 MW; 43CFDD4 CRC32;

Query Match 41.4%; Score 1244; DB 11; Length 558;
Best Local Similarity 42.7%; Pred. No. 2e-71;
Matches 243; Conservative 115; Mismatches 173; Indels 38; Gaps 12;
QY 22 HTDSAGRP-VFVPEOGG-----YKRFYKVEDKCKCEKCHLVLCSPKQTEGCH 70
Db 3 HSEQAAVPCAFIRONGNSISLDEPDTEYQFVEQLEERKCAFCHSVLNPHTGCGH 62
QY 71 RFCESCMAALIS-SSSPKTAQESIVKDFKDNCKREITLAIQYCRNRSRGAQOLM 129
Db 63 RFCQOCIRSLSELNSVPCIPVDKEVIRKQVFKDNCKREVLNHYCKN-APGCNARI 121
QY 130 LG-----HLVHLKNDCHFEELPCVRDCKEKLRLDLRDHVKACKYREATSHCKSOVPM 185
Db 122 LGRFDHLOH-----CSFOAVPCPNESCREAMLKRDVKEHLKSAVCFREKCLCYCKRDIV 177

QY 186 IALOKHEDTDCPVVSCPHKCSVOTLLRSELSEAHLSVCVNAFSTCSFRRYGCFTNQ 245
Db 178 TNLQDHEENSGPAIPVSCPNRC-VQITPRARVNHLYCPREABEDCFPKHGCIVKRG 236
QY 246 QIKAHKHAESSAVQHVWMLKEMNSLSLEKKSLLQNESEVENKKSIOSLHNOICSEI 305
Db 237 NLBHERAALQDHLVLLENKYQLEGRISDLYQSLQEKESKIQDLAETVKKFEKELQFT 296
QY 306 EMLNNEKSIHLQVIDSQAELKELDKETIRPFQONWEADSMKSSESLONR 359
Db 297 QMFGRNCTFJSMQ-ALTSHTDKSAMLEAQYROLQIVNOQPSRLDRLSLDAVDAYKOR 355
QY 360 VTELESVDKSGQVARTGLLESQLSRHDOMLSYHDIRLADMGLFOYLETASNGVLIW 419
Db 356 ITQLEASD-----QRLVLEGETSKDAHINHKQOLKNERNERFQLEAGACISGLI 408
QY 420 KIRYKRRKQAVNGKTLSTLSOPEFTYGFYKMCARYLNGDMGKTHLSLFFVIMRG 479
Db 409 KVTYRVRKRAVAGHIVSVSOPFTYSGCYRLCAAYLNGDSGKTHLSLFFVIMRG 468
QY 480 EYDALLPMPFKOKYTLMLMDGSSRRHLGDAFKPDPNSSFKPTGEMNINSGCPVFAQ 539
Db 469 EFDLQMPYRQVYTLMLMDGSKRNHIVETFKADPNSSFKPRDGEKNINSGCPVFAQ 528
QY 540 TVLEN--GTYIKDITFIKVIYDTSIDLPD 566
Db 529 STENSKNTYIKDITFIKVIYDTSIDLPD 557

RESULT 4
ID 061480 PRELIMINARY; PRT; 558 AA.
AC 061480;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TRAF5.
GN TRAF5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96278943.
RA NAKANO H., OSHIMA H., CHUNG W., WILLIAMS-ABBOTT L., WARE C.F.,
RY YAGITA H., OKUMURA K.;
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
the lymphotoxin-beta receptor.";
J. Biol. Chem. 271:14661-14664(1996).
-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL: D78141; BA11218.1; -
MGI: 107548; Traf5.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
DR PFM: PFO0917; MATH; 1.
DR PFM: PFO0097; Zf-C3HC4; 1.
KM Zinc-finger.
SQ SEQUENCE 558 AA; 64154 MW; 910ACC60 CRC32;

Query Match 41.4%; Score 1244; DB 11; Length 558;
Best Local Similarity 41.3%; Pred. No. 2e-71;
Matches 241; Conservative 113; Mismatches 163; Indels 66; Gaps 11;
QY 22 HTDSAGRP-VFVPEOGG-----YKRFYKVEDKCKCEKCHLVLCSPKQTEGCH 70
Db 3 HSEQAAVPCAFIRONGNSISLDEPDTEYQFVEQLEERKCAFCHSVLNPHTGCGH 62
QY 71 RFCESCMAALIS-SSSPKTAQESIVKDFKDNCKREITLAIQYCRNRSRGAQOLM 129
Db 63 RFCQOCIRSLSELNSVPCIPVDKEVIRKQVFKDNCKREVLNHYCKN-APGCNARI 121
QY 130 LG-----HLVHLKNDCHFEELPCVRDCKEKLRLDLRDHVKACKYREATSHCKSOVPM 185


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Db 122 IGRQDHLQ-----CSFOAVPCPNESCRAEMLRKDVKEHLSAYCRFBREKCLYCKRDIV 177
Qy 186 IALOKHEDTQPCVYVSCPHKCSVOTLLRSELNLSBVCVAPSTGSKRRGCVFQGNQ 245
Db 178 TNLQDHENSQPAYVSCPNBC-VQTLPRAVNEHLVYCPAEQDCPKHYKCTVKGKRG 236
Qy 246 QIRKASSAAYVNLKEMNSLEKVVSLQNSVEKNKSIOSLHNOICSEIEIEROK 305
Db 237 NLEHERAALQDHLVLEKRYOELQRIQSDLYQSLQEKESLQQLAEVYKFEKELQFT 296
Qy 306 EMLRNN-----ESKILHQRVIDSQAEKLEKELDEKPRQNMEE 345
Db 297 QMFRNGFTLSNVQALSHTDKSAWLEQVHRLQIVNQPSRL-----D 341
Qy 346 ADSKSSVESLQNVTELESVDKSAQVARNLTGLLESQLSRHQMLSVHDIRLADMQLG 405
Db 342 LRSILDVADSVKQRTQLEASD-----QKLVLEGETSKDHAINTHKQKLNKNERF 394
Qy 406 QVLEFASVNGVLYKIRIDYKRRKQEAVMGKTLSTYQPFYTGFGYKMCARVYLVGDMG 465
Db 395 KQLEGACVSGGLIMKVMYDQRYKREAVGHTVYVSQPFYTSRCGYRLCABAYLVGDMG 454
Qy 466 KGHLSLFTVIMRGEYDALPMPFRQKVTLMQOGSSRRHGLDAFKRDPNSSFKEKFTG 525
Db 455 KGHLSLFTVIMRGEYDALPMPFRQKVTLMQOGSSRRHGLDAFKRDPNSSFKEKFTG 514
Qy 526 EMTASGCPVFAQVTLN--GYIKDPTIFKIVYDTSQDLPD 566
Db 515 EMTASGCPVFAQVTLN--GYIKDPTIFKIVYDTSQDLPD 557
RESULT 5
ID 000463 PRELIMINARY: PRT: 557 AA.
AC 000463:
DT 01-JUL-1997 (TREMELREL. 04, Created)
DT 01-NOV-1998 (TREMELREL. 08, Last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, Last annotation update)
DE TRAF5 (TNF RECEPTOR ASSOCIATED FACTOR 5).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 9812745.
RA MITSUISHI S., FUJITA M., ISHIDA T., AZUMA S., KATO K., HIRAJI M.,
RA OTSUKA M., YAMAMOTO T., INOUE J.;
RA "Cloning and characterization of a cDNA encoding the human homolog of
tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998).
RN [2]
RP SEQUENCE OF 20-557 FROM N.A.
RX MEDLINE: 97321041.
RA NAKANO H., SHINDO M., YAMADA K., YOSHIDA M.C., SANTEE S.M., MARE C.F.,
RA JENKINS N.A., GILBERT D.J., YAGITA H., COPELAND N.G., OKUMURA K.;
RA "Human TNF receptor-associated factor 5 (TRAF5): cDNA cloning,
expression and assignment of the TRAF5 gene to chromosome 1q32.";
RL Genomics 42:26-32(1997).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: AB000509; BAA25262.1; -.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR PFM: PFO0917; MATH; 1.
DR PFM: PFO0097; ZF-C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 557 AA: 64405 MM; F46CAB2A CRC32;

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Query Match 39.3%; Score 1182; DB 4; Length 557;
 Best Local Similarity 41.6%; Pred. No. 1.7e-67;
 Matches .229; Conservative 121; Mismatches 181; Indels 20; Gaps 8;

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Qy 25 RSAGTPVFEVQGGYKKEFKYVEDKCYCKECHLVLCSPKQTCGHRFCSCMAALLS-S 83
Db 17 QNSGNSISLDEPSEIEQFPERLEERKCAFCBSVLNHPQTCGHRFCOCHLSLELN 76
Qy 84 SSPKCTACQESIYKDYKFNCKCKREILALQIYCRNESCABQMLGLVHLKNDCHF 143
Db 77 TVPICPVDEVIYSQEFKQNCCKREVLNLYVCSN-APCCNKKVILGRQDHLQCLFQ 135
Qy 144 ELPCVRDCKEYLRKDLRDHVERACKYREATCSQYPMALQKHEDTQPCVYVSC 203
Db 136 PVQCSNCKREPVLRKDLKEHLSASQCFRREKCLYCKKDVVAVINLQNHENLCEYVFC 195
Qy 204 PHKCVQTLRSELNLSBVCVAPSTGSKRRGCVFQGNQIKAHASAVQVNLK 263
Db 196 PNMCA-KITLKVDEHLAVCPAEQDCPKHYKCAVTDKRRNIQOHEHSAIRHMLVL 254
Qy 264 EMSNLEKRVSLQNSVEKNKSIOSLHNOICSEIEIEROKELRNESKILHQRVID 323
Db 255 EKNVQLEQISDLKLSLEQKESKIQQLAETIKRLEKFKQFAQLFGKNGSFLPNIQ-VFA 313
Qy 324 SQAEKLEKELKEIRPF-----RQNEBADMSKSSVESLQNVTELESVDKSAQVARN 377
Db 314 SHDKSAWLEQVHRLQIVNQOQNKEDLPRLMAVDTVQKITLLEND-----QRL 366
Qy 378 GLLESQLSRHQMLSVHDIRLADMQLGFOVLEFASVNGVLYKIRIDYKRRKQEAVMGKTL 437
Db 367 AVLEETNKDPTIFKIVYDTSQDLPD 426
Qy 438 SLYSQPFYTGFGYKMCARVYLVGDMGKGTLSLFTVIMRGEYDALPMPFRQKVTLM 497
Db 427 SIFQSFTLSGCRYRLCABAYLVGDMGSGSHLSLYFVMRGEYDALPMPFRQKVTLM 486
Qy 498 MDQSSRRHGLDAFKRDPNSSFKEKFTGEMNIAAGCPVFAQVTLN--GYIKDPTIF 555
Db 487 LDQ-SGKNIMETKPPDNSSSKFRPDGEMNIAAGCPVFAQVTLN--GYIKDPTIF 545
Qy 556 KVIYDTSQDLPD 566
Db 546 KVAVDLTLED 556

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RESULT 6
ID 054896 PRELIMINARY: PRT: 508 AA.
AC 054896:
DT 01-JUN-1998 (TREMELREL. 06, Created)
DT 01-JUN-1998 (TREMELREL. 06, Last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2A.
GN TRAF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=KIDNEY;
RX MEDLINE: 98129826.
RA BRINK R., LODISH H.F.;
RA "Tumor necrosis factor receptor (TNFR)-associated factor 2A (TRAF2),
a TRAF2 splice variant with an extended RING finger domain that
inhibits TNFR2-mediated NF-kappaB activation.";
RL J. Biol. Chem. 273:4129-4134(1998).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: AF027570; AAC53545.1; -.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR PFM: PFO0917; MATH; 1.
DR PFM: PFO0097; ZF-C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 508 AA: 56757 MM; 619B659E CRC32;

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Query Match 27.4%; Score 822.5; DB 11; Length 508;
 Best Local Similarity 33.6%; Pred. No. 8.6e-45;

Matches 199; Conservative 91; Mismatches 186; Indels 117; Gaps 21;

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Oy 3 SSKKSDSGALQTNPLKHLHDSAGTFFVPEQGYKEKPKT-VEDKYKCKHLYVC 61
Db 2 AAASVTSFSGSELLQP-----GFSKTLTGTLLEAKYLCISACKNTLR 42
Oy 62 SPKQTECGHRCESCM-----ALLSSSPK-CTAC-----QESI---VADKFFKNC 105
Db 43 RPFQACGCHRCFCLTJTLRCASITLSSSGPQNCACVYEGIEGISTLESSAFPDNA 102
Oy 106 KRETLALQIYCRNESCQAQMLGHLVHLKNDCHFEELPCVR--PDCKEVLKRDLR 162
Db 103 ARREVESLPAYCPND--GCTWK--GTLKEYES-CHGICLPFLLEPCAKGLVRLSEKE 156
Oy 163 DHEVACAKYREATCSCKSQVPMIALQKHEDTDCPCVYVSCPKKCSVQTLRLSELHAHS 222
Db 157 HHTDECKPRSLSCQHCAPCSHVDLEVHYEV-CPKFP LTC-DGCGKKRIPRETFQDHR 214
Oy 223 ECYNAPSTCSFRRYCGVGTNOQIKAHEDASSAVOHVNLKEMSNLEKVS----- 274
Db 215 ACSKRCVLCRHHVTCSEKVEVENLQDHELQRLREHLALL--LSSFLAQASPGTLNVOG 272
Oy 275 --LQNESVERKKSIOSLHNOICSEIEIEROKEMLRNNESTILHLOVYDSQAEKLEL 332
Db 273 PELQROQILBEQK-LATFENIVCVLNREVER-----VAVTAACSGRQHL 316
Oy 333 DKETRPFQONNEADSMKSSVESLQNRVTELESVDKSAGQVARNGLLESQLSRDQMS 392
Db 317 DOD-----KIEALSNKYQOLE-----RSIGL----- 337
Oy 393 VHDRLADMGLFOYLEETASVNGVLIMKIRDKRRKOEAVNMGKTLSTVSQPYTGFGYK 452
Db 398 -KDLMAADLEQKVSLESTVDGVTIMKISDFTKRQOEVAAGRTAITSAPATYSTRYGK 396
Oy 453 MCARYTLNGDGKNGKTHLSLFEVINGEYDALLPMPFKOKVYLMMDGSSRRHLGDAFK 512
Db 397 MCLARYTLNGDGTGRGTHLSLFEVYVVKGPNDALQMPFNQKVTMLLDH-NNREHYIDAFR 455
Oy 513 PDPNSSFRKPRGEMNINASGCPVFAQVYLE-NGTYIKDDTFFIVYDTSUL 564
Db 456 PDVYSSSFQRPVSDMNINASGCLFCPVSMEKANSYVRDALFIRAYDITGL 508

RESULT 7
Oy 012933 PRELIMINARY; PRT: 501 AA.
Db 012933;
Oy 01-NOV-1996 (TREMBLrel. 01, Created)
Db 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
Oy 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
Db 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
Oy TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3.
Db TRAP3.
Oy Homo sapiens (Human).
Db Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Oy Eutheria; Primates; Catarrhini; Homiidae; Homo.
Db [1]
Oy SEQUENCE FROM N.A.
Db MEDLINE; 95366958.
Oy SONG H.Y., DONNER D.B.;
Db MEDLINE; 94349371.
Oy ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;
Db "A novel family of putative signal transducers associated with the
Oy cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
Db Cell 78:661-692(1994).
Oy [3]
Db SEQUENCE FROM N.A.
Oy SONG H.Y.;
Db Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.

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CC -I- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: U12597; AA87706.1;
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 2.
DR PFAM; PF00917; MATH; 1.
DR PFAM; PF00097; ZI-C3HC4; 1.
DR Zinc-finger.
SQ SEQUENCE 501 AA; 55794 MW; 1C62BC1F CRC32;

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Query Match 24.58; Score 735.5; DB 4; Length 501;
 Best Local Similarity 33.68; Pred. No. 2,7e-39;
 Matches 187; Conservative 87; Mismatches 185; Indels 97; Gaps 22;

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Oy 36 QGGYKEKPKT-VEDKYKCKHLYLCSFKQTECHRCESCMALLSSSKCTAC-QE 93
Db 16 QGFESKTLTGTLLEAKYLCISACKNTLRPFQACGCHRCFCLTJTLRCASITLSSSGPQNCACVYH 75
Oy 94 SIYKDY-----FKDNCKRETLALQIYCRNESCQAQMLGHLVHLKNDCHFEEL 145
Db 76 GIEEGISILSSSAFPDNNARREVESLPAYC--PSDCTWK--GTLKEYES-CHGRC 129
Oy 146 PCVR--PDCKEVLKRDLDHEVACAKYREATCSCKSQVPMIALQKHEDTDCPCVYVS 202
Db 130 PLMLTECPACGLVRLGKERHLEHECPERSLSCHRCAPCCGADVKAHNEY-CPKFLT 188
Oy 203 CPKCSVQTLRLSELHAHSLESCYNAPSTCSFKRYGV--FGTNOQIARHESSAVOHVN 260
Db 189 C-DGCGKKRIPRETFQDHRVKTGCRVPCRFHALJCLTVEGEKQ--EHEVQMLREHLA 245
Oy 261 LKEWNSLEKK-----VSLQD-ESYERKKSIOSLHNOICSEIEIEROKEMLR 309
Db 246 ML--LSSYLEAKPPLDGDSHAGSELLQRCESLEKTA--TENTIVCVLNREVER----- 295
Oy 310 NNESTILHLOVYDSQAEKLELDEKIRPFQONNEADSMKSSVESLQNRVTELESVDKS 369
Db 296 -----VAMTAACSGRQHL-----KIRALSSKYQOLE----- 325
Oy 370 AGQVARNGLLESQLSRDQMSVNDIRLADMGLFOYLEETASVNGVLIMKIRDKRRKQ 429
Db 326 -----RSIGL-----KDLMAADLEQKVSLESTVDGVTIMKISDFTKRQOEVAAGRTAITSAPATYSTRYGK 366
Oy 430 EAVMGKTLSTVSQPYTGFGYKMCARYTLNGDGKNGKTHLSLFEVINGEYDALLPMPF 489
Db 367 EAVAGRIPIAITSAPATYSTRYGKMCARYTLNGDGKNGKTHLSLFEVYVVKGPNDALQMPFNQKVTMLLDH-NNREHYIDAFR 426
Oy 490 KQKVTLMMDGSSRRHLGDAFKPDPNSSFRKPRGEMNINASGCPVFAQVYLE-NGTYI 548
Db 427 NQKVTLMMDQ-NNREHYIDAFRDPVYSSSFQRPVSDMNINASGCLFCPVSMEKANSYV 485
Oy 549 KDDTFFIVYDTSUL 564
Db 486 RDDALFIRAYDITGL 501

RESULT 8
Oy 013077 PRELIMINARY; PRT: 416 AA.
Db 013077;
Oy 01-NOV-1996 (TREMBLrel. 01, Created)
Db 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
Oy 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
Db 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
Oy EPSTEIN-BARR VIRUS-INDUCED PROTEIN.
Db Homo sapiens (Human).
Oy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Oy Eutheria; Primates; Catarrhini; Homiidae; Homo.
Db [1]
Oy SEQUENCE FROM N.A.
Db TISSUE-TYMPHOID TUMOR;
Oy MOSTALOS G., BIRKENBACH M., VALAMANCHILI R., VANARSADALE T., WARE C.,
Db KIEFF E.;
Oy EMBL; U19261; AAA62309.1;
Db PFAM; PF00917; MATH; 1.

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SEQUENCE 416 AA; 46163 MM; 760442EC CRC32;

Query Match 21.2%; Score 637.5; DB 4; Length 416;
Best Local Similarity 35.3%; Pred. No. 3.5e-33;
Matches 164; Conservative 72; Mismatches 126; Indels 103; Gaps 17;

137 KNDCHFEELPCVRPOCKEVILKDLRDHYERKACKYREATCSHQVPMIALQKHEDTDC 196
15 ENDFPGCPPTCQDPKEP-----RALCCAGCJSENP-----RNGEDDIC 54
197 PCVVASCPRKCSYQVL-----LRSELSAHLSECVNAPSTCSKRRKCGVCGOQNOIK 248
55 P-----KCREGDLQSIKSGRLRTOEKAN-PEVAEKGICCPVAGVCSFKSPQSVQ 105
249 AHEASSAVOHVNL-----KEMS-----NSLEKVSLLQ-NESEYKKSQ-SLH 291
106 EHEVTQSOTSHNLILGFMKQWKARLCCGLESQPMALQOLQANVAGDLEVDY 165
292 NOJCSFEIEROKEMLRNNEKILHQRVIDSOAEKLELDEKLEIRPQNNEADSKMS 351
166 RAPCS-----ESQEE-----LALQHPM--KEKILAELEKILRVF-----E 198
352 SVESLQNRVTELESVDKSAQVARNGLLESOLSRH-----DOMLSVHDIRLA 399
199 NIVAVLNKREVE-----ASHLALATSIHOSOLDREIRILSEQRVVELQOTLAOKDOALG 251
400 DMDGFOVLETASYNGVILNKIRIDYKRRKQDAVNGKTLISYQPTTGYGYKMCARVYL 459
252 KLEOSLRIMEASPDGFEIKRITVTRCHESACGRVTSLESPFAFYAKYGLCLRLYL 311
460 NGDGMKGKTHLSLFVYIRGEYDALLPMPFKOKVTLMMDGSSRRHLDGAFKPPDNSSS 519
312 NGDGTGKTRTHLSLFVYIRGEYDALLPMPFRNKVTFPHLLQO-NRREHAIADAFRDLSAS 370
520 FKPTGEMNINASGCPVEFAQTVLEN--GTVIKDDITFIKVIYDTS 562
371 FQRPQSETNINASGCLFFPLSLKSGPKHAYVKDDTMFKICIVETS 415

RESULT 9
OQYAK3 PRELIMINARY; PRT; 522 AA.
ID OQYAK3:
AC 01-NOV-1996 (TREMBLrel. 12, Created)
DT 01-NOV-1996 (TREMBLrel. 12, last sequence update)
DE 01-NOV-1996 (TREMBLrel. 12, last annotation update)
DE PUTATIVE INTERLEUKIN 1 SIGNAL TRANSDUCER.
TRAFF.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
SEQUENCE FROM N.A.
RP MEDLINE: 96434692.
RX CNO 2., XIONG J., TAKEUCHI M., KURAMA T., GOEDDEL D.V.;
RA "RA6 is a signal transducer for interleukin-1."
RT Nature 383:443-446(1996).
CC EMBL: U78798; AAB38751.1; -
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR ZINC-FINGER.
KW ZINC-FINGER.
SEQUENCE 522 AA; 59573 MM; AE59362 CRC32;

Query Match 18.5%; Score 554.5; DB 4; Length 522;
Best Local Similarity 26.5%; Pred. No. 8.3e-28;
Matches 143; Conservative 101; Mismatches 200; Indels 95; Gaps 15;
32 FVPEQGGKREKFKVTKVEKCKECHKHVLKSPKQEGHRCESCMALISSSPKCTAC 91
49 FMEELQGYDVEFDPPLPEKTECPICLMLADREAVOTPCGHRCKKACIIKSINDAGHKCPVD 108

92 QESTVDRVFQDNCKREITLALQITCRNBSRGCAEOLMGLHVLKNDCHFEELPCVRPD 151
109 NEILLNQLEFPDNFAKREILSLAWKPN--GCLKNELNHLHDHQAHCFAALMDC--PQ 164
152 CKEVLRKDLNDHYERKACKYREATCSHQVPMIALQKHEDTDCPCVVASCPRKCSYQV 211
165 CQRPQKHINHLKDCPRQVSDONAAAMAREDEKH--DONCPLANVCEY-CNT-1 221
212 LRSELSAHL--ECVNAPSTCSFKRYGCVFOGTNOQKAHEASSAVOHVNLKEMSNLE 270
222 LIREQMPNHYDDCPAPICPTFTFGCHERQNRNHLARHLEQNTOSHMRLAQAVSL- 280
271 KAVSLQNSVEKNSISLHNOCSFEIEROKEMLRNNEKILHQRVIDSOAEKLEK 330
281 -----SVIPDSGIS--EVNRFQETIHQLEGRVLDHQRHRELTAKMETOSMTVS 328
331 ELDEIRPFRQNEADSKMSVSELSQNRVTELESVDKSAQVARNGLLESOLSRHDM 390
329 ELKRTIR-----TLEKVAEIEA----- 346
391 LSVHDIRLADMDIGFOVLETASYNGVILNKIRDY-----KRRKQDAVNGKTLISYQPTT 446
347 -----QCCNGIYINKIGFQHNLKQEEB--KPVVISHPGEYT 382
447 GYFGKRCARVYLN-GDGMKGKTHLSLFVYIRGEYDALLPMPFKOKVTLMMDGSS-- 503
383 GKPKYKLCMLHLQPLAQRCAVYISLFTVMQGEDSHLPWFQGTIRLITLIDSEAPV 442
504 RRLHGDAPKPPDNSSSPKRPTEGEMNINAS--GCPVEFAQTVLENGYIKDDITFIKVIYD 561
443 RQNHLEIMDARPELLARQRTIPRNPFGFYTFMHLALRQGTIKDDITLAVCEVST 501

RESULT 10
ID Q14848 PRELIMINARY; PRT; 470 AA.
AC Q14848:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-NOV-1996 (TREMBLrel. 12, last annotation update)
DE CYSTEIN RICH DOMAIN ASSOCIATED TO RING AND TRAF PROTEIN.
MLN 62, CARL.
GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
SEQUENCE FROM N.A.
RP TISSUE-BREAST DERIVED METASTATIC LYMPH NODE.
RC MEDLINE: 96039245.
RX TOMASETO C., REGNIER C.H., MOOG-LUTZ C., MATTEI M.G., CHENARD M.P.,
RA TOMASETO C., REGNIER C.H., MOOG-LUTZ C., MATTEI M.G., CHENARD M.P.,
RA LIDEREAU R., BASSET P., RIO M.C.;
RT "Identification of four novel human genes amplified and overexpressed
RT in breast carcinoma and localized to the q11-q21.3 region of
RT chromosome 17."
RT Genomics 28:367-376(1995).
RL
RN
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST DERIVED METASTATIC LYMPH NODE;
RX MEDLINE: 96029665.
RA REGNIER C.H., TOMASETO C., MOOG-LUTZ C., CHENARD M.P., WENDLING C.,
RA BASSET P., RIO M.C.;
RT "Presence of a new conserved domain in CARL, a novel member of the
RT tumor necrosis factor receptor-associated protein family, which is
RT expressed in breast carcinoma."
RL J. Biol. Chem. 270:25715-25721(1995).
CC EMBL: X80200; CA556491.1; -
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR PFAM: PF00917; MATH; 1.
DR PFAM: PF00097; ZF-C3HC4; 1.
KW ZINC-FINGER.
SEQUENCE 470 AA; 53443 MM; F3B78A90 CRC32;

Db	181	SQVMIALQKHEDHDCCVYVSCCHKRSVOTLIRSELSAHLSBVCVNPAPISCFKRRKGCVF	240
Qy	241	QGTNOQIKAHEBASSAVOHVNLKLEKWSNLSLEKRVSLQNESVEKNKSISQJLHNOICSEFEI	300
Db	241	QGTNOQIKAHEBASSAVOHVNLKLEKWSNLSLEKRVSLQNESVEKNKSISQJLHNOICSEFEI	300
Qy	301	IEROKEMLRNNESKILHLQVRIDSOAERKLELKEIIRPFROBNWEADSMSSVESJLONRY	360
Db	301	IEROKEMLRNNESKILHLQVRIDSOAERKLELKEIIRPFROBNWEADSMSSVESJLONRY	360
Qy	361	TELESVDKSAGOVARNRTGILESQLSRHDOMLSVNDIDILADMDLGFVYLETASYNGVLIWK	420
Db	361	TELESVDKSAGOVARNRTGILESQLSRHDOMLSVNDIDILADMDLGFVYLETASYNGVLIWK	420
Qy	421	IRDYKRRKQEAVMGKTJLSYSQPFYTGIFGFKWCARVYLYNGDGMGKTHLSLFFVIMRGE	480
Db	421	IRDYKRRKQEAVMGKTJLSYSQPFYTGIFGFKWCARVYLYNGDGMGKTHLSLFFVIMRGE	480
Qy	481	YDALLPWFKRYVLLMLMDGSSSRHHJGDAPKPDPNSSSFRKKPFGEMNIIASGCPVFAQOT	540
Db	481	YDALLPWFKRYVLLMLMDGSSSRHHJGDAPKPDPNSSSFRKKPFGEMNIIASGCPVFAQOT	540
Qy	541	VLENGTYIKDDTIFIKVIVDSDPDP	567
Db	541	VLENGTYIKDDTIFIKVIVDSDPDP	567

RESULT	2
ID	W03146
AC	W03146 standard; protein; 568 AA.
DT	23-Oct-1996 (first entry)
DE	LMPI associated protein LMPI.
KW	LMPI; LMPI associated protein 1; latent infection membrane protein;
KW	tumour necrosis factor receptor associated factor; TRAF;
KW	signal transduction; TNF; TNFR; lymphoblast; tumorigenesis; AIDS;
KW	Hodgkin's disease; Burkitt's lymphoma; nasopharyngeal carcinoma;
KW	mononucleosis; Epstein-Barr virus; EBV; therapy.
OS	Homo sapiens.
FH	Key
FT	Location/Qualifiers
FT	/label= LMPI-Binding_domain
FT	309..341
FT	/label= Coiled_coil_domain
FT	406..568
FT	/label= Carboxy-terminal domain
FT	
PN	W09620723-A1.
PD	11-JUL-1996.
PF	28-DEC-1995; U16980.
PF	30-DEC-1994; US-67540.
PM	(BGHM) BRIGHAM & WOMENS HOSPITAL.
PM	(REGC) UNIV CALIFORNIA.
PT	Birkenbach M, Kaye KM, Kieff E, Mosialos G, Vanarsdale T;
PT	Ware CJ
PT	WPI; 96-333765/23.
DR	N-PSDB: T31273.
PT	Compounds and methods for controlling TRAF-mediated signals - by
PT	modulating interactions between Epstein Barr virus encoded proteins
PT	LMPI, LMPI, TNF, TNFR to inhibit lymphoblast growth and
PT	tumorigenesis.
PS	Claim 74: Page 58-60: 87pp: English.
CC	A novel human B-cell protein (W03146), termed LMPI associated protein
CC	1 or LMPI, strongly associates with the cytoplasmic C-terminal domain
CC	1 (LMPI), a domain that is stringently required for transformed cell
CC	growth. LMPI is related to murine tumour necrosis factor receptor
CC	associated factor TRAF2. A related novel B-cell protein (W03147),
CC	EBI6, appears to be the human homologue of murine TRAF1. LMPI
CC	polypeptides, esp. the LMPI binding domain, coiled coil domain and
CC	C-terminal domain can be used to inhibit LMPI-TRAF interaction.
CC	Such polypeptides, which may be obt. by recombinant means (see
CC	also T31273) can be used to treat infection and control cell growth
CC	or tumorigenesis associated with LMPI-encoding viruses, partic. EBV

Seq	Sequence	568 AA:	Query Match	99.4%:	Score 2986.5:	DB 1:	Length 568:
			Best Local Similarity	99.6%:	Pred. No. 3e-227:		
			Matches 566:	Conservative	0:	Mismatches 1:	Indels 1:
						Gaps	
QY	1	MESSKKMDSPALQTNPLKLTHTDRSAGTVFVPEQGGYKEKEFKVTEYDKYCKECHLYL	60				
DB	1	MESSKKMDSPALQTNPLKLTHTDRSAGTVFVPEQGGYKEKEFKVTEYDKYCKECHLYL	60				
QY	61	CSPKTEGCHGFHCSSCAALILSSSPCTCAQESIVADKYFKDNCKCKRELLAQICRNE	120				
DB	61	CSPKTEGCHGFHCSSCAALILSSSPCTCAQESIVADKYFKDNCKCKRELLAQICRNE	120				
QY	121	SRGCAEQQLMGLH-LVHLKNDCHFELPCVPDPCKEKYLRKDLRDHYEKACKYREATCSHC	179				
DB	121	SRGCAEQQLMGLHLYHLKNDCHFELPCVPDPCKEKYLRKDLRDHYEKACKYREATCSHC	180				
QY	180	KSQVPMILQKHEDTDCPVVYVSCPCHKCSVQTLIRSELSHLSVCYVAPSTCSFKRGCY	239				
DB	181	KSQVPMILQKHEDTDCPVVYVSCPCHKCSVQTLIRSELSHLSVCYVAPSTCSFKRGCY	240				
QY	240	FOGTNOQIKAEHSAVAOVHMLKEMSNLSLEKTVSLLOÑESVEKKNKSIOSLHNOICFEL	299				
DB	241	FOGTNOQIKAEHSAVAOVHMLKEMSNLSLEKTVSLLOÑESVEKKNKSIOSLHNOICFEL	300				
QY	300	ETEROKEMLRNÑESKIHLQAVIDSOAEKLKELDKETIRPRÖNWEEDSMKSVESIQNR	359				
DB	301	ETEROKEMLRNÑESKIHLQAVIDSOAEKLKELDKETIRPRÖNWEEDSMKSVESIQNR	360				
QY	360	VTELESVKSAGOVARNITGLLESOLSHRDQMLSVYHDIRLADMGLGFOVLETASYNGYLW	419				
DB	361	VTELESVKSAGOVARNITGLLESOLSHRDQMLSVYHDIRLADMGLGFOVLETASYNGYLW	420				
QY	420	KTRDYKRRKQEAVMGKTLISLSQPFYTYGFEYKKACARVYLANGDMGNGTSLSFVIMRG	479				
DB	421	KTRDYKRRKQEAVMGKTLISLSQPFYTYGFEYKKACARVYLANGDMGNGTSLSFVIMRG	480				
QY	480	EYDALLPMPFKOKVYLMIMDGGSSRRHLGDAFKDPDPSSSFKKPTGEMINIASGCPYVAQ	539				
DB	481	EYDALLPMPFKOKVYLMIMDGGSSRRHLGDAFKDPDPSSSFKKPTGEMINIASGCPYVAQ	540				
QY	540	TYLENGYTIKDDTIFIKYIVVTSLLPDP	567				
DB	541	TYLENGYTIKDDTIFIKYIVVTSLLPDP	568				

RESULT	3
ID	W27431
AC	W27431 standard; Protein; 568 AA.
DT	W27431.
DE	27-MAR-1998 (first entry)
KW	Human CRAF1-a (TRAF-3-p55) polypeptide.
KW	CD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human;
KW	CD40 mediated intracellular signalling; organ rejection; allergy;
KW	hay fever; autoimmune disease; systemic lupus erythematosus;
KW	rheumatoid arthritis; myasthenia gravis; Graves' disease;
KW	idiopathic thrombocytopenia purpura; haemolytic anaemia;
KW	diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
KW	apoptosis; Rieter's syndrome; spondyloarthritis; Lyme disease; HIV;
KW	syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
KW	pneumoconiosis; adult respiratory distress syndrome; pneumonitis;
KW	asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
KW	atherosclerosis; multiple sclerosis; glomerulonephritis;
KW	glomerulosclerosis; glomerulopathy; kidney disease; nephropathy;
KW	endocarditis; leprosy; malaria; Goodpasture's disease;
KW	Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
KW	Wegener's granulomatosis; cryoglobulinemia;
KW	Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
KW	AIDS; oesophageal dysmotility; inflammatory bowel disease;
KW	bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
KW	Darvall's lymphoma; nasopharyngeal carcinoma; pneumonia.

FT Region 330, His-343 and Cys-347)"

FT /note= "zinc finger 5 (Zn binding to Cys-354,

FT Cys-361, His-373 and His-381"

FT Binding_site 16.19

FT /note= "putative SH3 binding motif"

FT Binding_site 44.47

FT /note= "putative SH3 binding motif"

FT Binding_site 103.110

FT /note= "putative SH3 binding motif"

PN W09734473-A1.

PD 25-SEP-1997. U05076.

PR 21-MAR-1997: US-026584.

PR 18-SEP-1996: US-013820.

PR 21-MAR-1996: US-013820.

PR 01-MAY-1996: US-016626.

PR 01-MAY-1996: US-016659.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Cleary AM, Frank DM, Lederman S;

PI WPI: 97-479907/44.

DR N-PSDB: T90123.

CC This polypeptide comprises a CRAF1 (TRAF-3) protein designated

CC CRAF1-b or TRAF-3-p70 or p70 or CRAF1(p70) or TRAF-3(p70). It

CC is encoded by exons 1-2 and 4-13 of the human CRAF gene (see

CC W27432). A lower mol.wt. CRAF1, designated CRAF1a (see W27431), has

CC also been identified, as well as isoforms p5 (see W27429), p15 (see

CC W27430) and variants of CRAF-1a and CRAF-b (see W27432-37) that

CC comprise different combinations of zinc fingers. CRAF1 peptides,

CC comprising from 0-4 zinc finger domains, and nucleic acids encoding

CC them, can be used to inhibit CD40 ligand activation of cells that

CC express CD40 on their surface, particularly by introducing the

CC nucleic acid molecule into the cells, useful to treat conditions

CC characterised by an aberrant or unwanted level of CD40 mediated

CC intracellular signalling, such as organ rejection, or a CD40

CC dependent immune response in a subject receiving gene therapy. The

CC condition may be an allergic response or an autoimmune response, or

CC may be dependent on CD40 ligand-induced activation of epithelial

CC cells, an inflammatory kidney disease, a smooth muscle cell-

CC dependent disease, or a condition associated with Epstein-Barr

CC virus.

CC Sequence 690 AA:

QY Query Match 99.2%; Score 2980.5; DB 1; Length 690;

QY Best Local Similarity 99.5%; Pred. No. 1.2e-226;

QY Matches 565; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

DB 1 MESSKRMDSFGALQTNPLKLTDRSAGTPVFPDGGKKEKFTVTEDEKICECHYL 60

DB 123 MESSKRMDSFGALQTNPLKLTDRSAGTPVFPDGGKKEKFTVTEDEKICECHYL 182

QY 61 CSPKQTEGHRCESCMAALSSSSPKTACQESIVKQVFQDNCKKRIIALQIYCRNE 120

DB 183 CSPKQTEGHRCESCMAALSSSSPKTACQESIVKQVFQDNCKKRIIALQIYCRNE 242

QY 121 SRGCAEQLMLGH-LVHLKNDCHFEELPCVRPDKCKEVLAKDLRDHYERACKYREATCSHC 179

DB 243 SRGCAEQLMLGH-LVHLKNDCHFEELPCVRPDKCKEVLAKDLRDHYERACKYREATCSHC 302

QY 180 KSOVPMALQKREDTDCPCVVVSCCHKSCVQTLNLSELSAHSECVNAPSTCSFRYGCY 239

DB 303 KSOVPMALQKREDTDCPCVVVSCCHKSCVQTLNLSELSAHSECVNAPSTCSFRYGCY 362

QY 240 FQGTNOQIKAHASSAYOVNLTKEVNSLEKVSILQNESEKKNKSIOSLNQCISFEI 299

DB 363 FQGTNOQIKAHASSAYOVNLTKEVNSLEKVSILQNESEKKNKSIOSLNQCISFEI 422

QY 300 EIEROKEMLRNNSKITLHQRVIDSOAEKLEKDEIRPFQRMWEADSMKSSVESLQNR 359

DB 423 EIEROKEMLRNNSKITLHQRVIDSOAEKLEKDEIRPFQRMWEADSMKSSVESLQNR 482

QY 360 VTELESYDKAGQVARTGLLESQLSRHQOMLSVNHRIADMDLGRQVETASTYNVLW 419

DB 483 VTELESYDKAGQVARTGLLESQLSRHQOMLSVNHRIADMDLGRQVETASTYNVLW 542

QY 420 KIRDYKRKQEAVMGKTLISQPFYTGFGYKRCARVYLNGDMGKGTLSLFFYIMRG 479

DB 543 KIRDYKRKQEAVMGKTLISQPFYTGFGYKRCARVYLNGDMGKGTLSLFFYIMRG 602

QY 480 EYDALLPMPKQAVTLMMDQSSRRHLGDAFKPDNSSSFKKPTGEMNTIASCPIVVAQ 539

DB 603 EYDALLPMPKQAVTLMMDQSSRRHLGDAFKPDNSSSFKKPTGEMNTIASCPIVVAQ 662

QY 540 TVLENGTYIKDDTFFIKVIYDTSQDPDP 567

DB 663 TVLENGTYIKDDTFFIKVIYDTSQDPDP 690

RESULT 5

W27432

ID W27432 standard: Protein; 543 AA.

AC W27432;

DT 27-MAR-1998 (first entry)

DE Human CRAF1 isoform p55del19.

KW CD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human;

KW CD40 mediated intracellular signalling; organ rejection; allergy;

KW hay fever; autoimmune disease; systemic lupus erythematosus;

KW rheumatoid arthritis; myasthenia gravis; Graves' disease;

KW idiopathic thrombocytopenia purpura; haemolytic anaemia;

KW diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;

KW apoptosis; Rietter's syndrome; spondyloarthritis; Lyme disease; HIV;

KW syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;

KW pneumococcosis; adult respiratory distress syndrome; pneumonitis;

KW asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;

KW atherosclerosis; multiple sclerosis; glomerulonephritis;

KW glomerulosclerosis; glomerulopathy; kidney disease; nephropathy;

KW endocarditis; leprosy; malaria; Goodpasture's disease;

KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;

KW Wegener's granulomatosis; cryoglobulinemia; amyloidosis; Sjogren's syndrome;

KW Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;

KW AIDS; oesophageal dysmotility; inflammatory bowel disease;

KW bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;

KW Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;

KW gene therapy; diagnosis.

OS Homo sapiens.

FT Region 117.141

FT /note= "zinc finger 1 (Zn binding to Cys-117,

FT Cys-124, His-136 and Cys-141)"

FT Region 148.170

FT /note= "zinc finger 2 (zinc binding to Cys-148,

FT Cys-153, His-165 and Cys-170"

FT Region 177.197

FT /note= "zinc finger 3 (Zn binding to Cys-177,

FT Cys-180, His-192 and Cys-197"

PN W09734473-A1.

PD 25-SEP-1997. U05076.

PR 21-MAR-1997: US-026584.

PR 18-SEP-1996: US-013820.

PR 21-MAR-1996: US-013820.

PR 01-MAY-1996: US-016626.

PR 01-MAY-1996: US-016659.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Cleary AM, Frank DM, Lederman S;

PI WPI: 97-479907/44.

DR N-PSDB: T90123.

CC This polypeptide comprises a CRAF1-b domain capable of inhibiting CD40

CC mediated cell activation - useful to treat conditions characterised

CC by aberrant or unwanted level of CD40 mediated intracellular

CC signalling

CC Example 1; Fig 1d-o; 158pp; English.

CC This polypeptide comprises a CRAFT (TRAF-3) isoform designated
CC p55d19. It is encoded by exons 4-8 and 10-13 of the human CRAFT
CC gene (see T50123) and arises by alternative splicing of the
CC sequence for CRAFT- α (see W27431), a signalling protein that
CC interacts with the cytoplasmic tail of a B cell surface molecule CD40
CC and which mediates a variety of T-dependent effects on B cell
CC activation and differentiation. A higher mol.wt. CRAFT, designated
CC CRAFT β (see W27428), has also been identified, as well as isoforms
CC p5 (see W27429), p15 (see W27430) and variants of CRAFT- α and
CC CRAFT- β (see W27432-37) that comprise different combinations of 5
CC zinc fingers. CRAFT peptides, comprising from 0-4 zinc finger
CC domains, and nucleic acids encoding them, can be used to inhibit
CC CD40 ligand activation of cells that express CD40 on their surface,
CC particularly by introducing a nucleic acid molecule into the cells,
CC and used to treat conditions characterised by an aberrant or
CC unwanted level of CD40 mediated intracellular signalling, such as
CC organ rejection, or a CD40 dependent immune response in a subject
CC receiving gene therapy. The condition may be an allergic response
CC or an autoimmune response, or may be dependent on CD40 ligand-
CC induced activation of epithelial cells, an inflammatory kidney
CC disease, a smooth muscle cell-viral disease, or a condition
CC associated with Epstein-Barr virus.

Sequence 543 AA;

Query Match	93.8%	Score 2820	DB 1	Length 543
Best Local Similarity	95.1%	Pred. NO. 3.7e-214		
Matches 540	Conservative	0	Mismatches 2	Indels 26
				Gaps 2

QY	1	MESSKKNDSPALQTNPPKLTHTRSAGTPAEVQEGCYEKFKPYVEDYKCKCHLVL	60
Db	1	MESSKKNDSPALQTNPPKLTHTRSAGTPAEVQEGCYEKFKPYVEDYKCKCHLVL	60
QY	61	CSFKQTEGHRFCESCAALLSSSPKCTACQESIVDKYVFKDNCCKREILTAQIYCRNE	120
Db	61	CSFKQTEGHRFCESCAALLSSSPKCTACQESIVDKYVFKDNCCKREILTAQIYCRNE	120
QY	121	SRGCAEQTLMLGCH-LVYHLKNDCHFELPCVPRDCKEYVLRDLRDRHYKACKYREATCSHC	179
Db	121	SRGCAEQTLMLGCHLVYHLKNDCHFELPCVPRDCKEYVLRDLRDRHYKACKYREATCSHC	180
QY	180	KSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLILSELSAHLSECYNAPSTCSFKRYGCV	239
Db	181	KSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLILSEL-----	217
QY	240	FQGNQOIKKAEASAAVOHVLKLEWNSLLEKKVSLLOÑESVEKNKSIOSLHNOICFEEI	239
Db	218	--GÑIOQIKKAEASAAVOHVLKLEWNSLLEKKVSLLOÑESVEKNKSIOSLHNOICFEEI	275
QY	300	EIERQKEMLRNNESEKILHLQVRIDSOAEKLELDEKIRPRQWNEADSMKSVSYESLQNR	359
Db	276	EIERQKEMLRNNESEKILHLQVRIDSOAEKLELDEKIRPRQWNEADSMKSVSYESLQNR	335
QY	360	VTELESYDKSAGOVARNTGILLESOLSRHDDMLSVHDIRLMDMOIGFQVLTASVNGVLIV	419
Db	336	VTELESYDKSAGOVARNTGILLESOLSRHDDMLSVHDIRLMDMDRQVLETAISINGVLIV	
QY	420	KIRDYKRRKQDAVNGKTLISYQPFYTGFGYKKACAVYLINGDGMGKGTLSLFEVIMRG	479
Db	396	KIRDYKRRKQDAVNGKTLISYQPFYTGFGYKKACAVYLINGDGMGKGTLSLFEVIMRG	455
QY	480	EYDALLMPFPQOKYTLMLDMOGSSRRHLHGAPFRVDPNSSFKKPKTGEMNTASGCPVYVQ	539
Db	456	EYDALLMPFPQOKYTLMLDMOGSSRRHLHGAPFRVDPNSSFKKPKTGEMNTASGCPVYVQ	515
QY	540	TVLENGYIKKDIITFIKVIYVDTSDLPPD	567
Db	516	TVLENGYIKKDIITFIKVIYVDTSDLPPD	543
RESULT	6		
W27433			
ID	W27433	standard; Protein; 665 AA.	

RESULT	6
W27433	
ID	W27433 standard; Protein; 665 AA

AC	W27433:	(first entry)
DE	27-MAR-1998	
KW	Human CRAF1-b isoform p70del9.	
KW	CD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human;	
KW	CD40 mediated intracellular signalling; organ rejection; allergy;	
KW	hay fever; autoimmune disease; systemic lupus erythematosus;	
KW	rheumatoid arthritis; myasthenia gravis; Graves' disease;	
KW	idiopathic thrombocytopenia purpura; haemolytic anaemia;	
KW	diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;	
KW	apoptosis; Riley's syndrome; spondyloarthritis; Lyme disease; HIV;	
KW	syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;	
KW	pneumococcal; adult respiratory distress syndrome; pneumonitis;	
KW	abestrosis; silicosis; Farmer's lung; hepatitis; cirrhosis;	
KW	atherosclerosis; multiple sclerosis; glomerulonephritis;	
KW	glomerulonephritis; glomerulopathy; kidney disease; nephropathy;	
KW	endocarditis; leprosy; malaria; Goodpasture's disease;	
KW	Henoch-Schönlein purpura; polyarteritis; multiple myeloma;	
KW	Megener's granulomatosis; cryoglobulinemia; amyloidosis; Sjögren's syndrome;	
KW	Waldenstrom's macroglobulinemia; amyloidosis; Sjögren's syndrome;	
KW	AIDS; oesophageal dysmotility; inflammatory bowel disease;	
KW	Burkitt's disease; Epstein-Barr virus; mononucleosis; B cell tumour;	
KW	Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;	
OS	Home sapiens.	
EH	Key	Location/Qualifiers
FT	Domain	52..122
FT		/label="CRAF-b_domain
FT		/note="Claim 1"
FT	Region	239..263
FT		/note="zinc finger 1 (Zn binding to Cys-239,
FT		Cys-246, His-258 and Cys-263)"
FT	Region	270..292
FT		/note="zinc finger 2 (zinc binding to Cys-270,
FT		Cys-275, His-287 and Cys-292 "
FT	Region	299..319
FT		/note="zinc finger 3 (Zn binding to Cys-299,
FT		Cys-302, His-314 and Cys-319"
FT	Binding-site	16..19
FT		/note="putative SH3 binding motif"
FT	Binding-site	44..47
FT		/note="putative SH3 binding motif"
FT	Binding-site	103..110
FT		/note="putative SH3 binding motif"
PN	MO9734473-A1.	
PD	25-SEP-1997.	
PR	21-MAR-1997; US05076.	
PR	18-SEP-1996; US-026584.	
PR	21-MAR-1996; US-013820.	
PR	01-MAY-1996; US-016626.	
PR	01-MAY-1996; US-016659.	
PA	(UYCO) UNIV COLUMBIA NEW YORK.	
PI	Cleary AM, Frank DM, Lederman S;	
DR	WPI, 97-479907/44.	
DR	N-PDB: T90123.	
PT	protein comprising CRAF1-b domain capable of inhibiting CD40	
PT	mediated cell activation - useful to treat conditions characterised	
PT	by aberrant or unwanted level of CD40 mediated intracellular	
PT	signalling	
PS	Example 1; Fig 1A-O; 158pp; English.	
CC	This polypeptide comprises a CRAF1 (TRAF-3) protein designated	
CC	p70del9 that is encoded by exons 1-2, 4-8 and 10-13 of the human	
CC	CRAF gene (see T90123). Different isoforms (W27428-37) of CRAF1	
CC	have been identified that arise from alternative splicing. CRAF1	
CC	peptides comprising from 0-4 zinc finger domains, and nucleic acids	
CC	encoding them, can be used to inhibit CD40 ligand activation of	
CC	cells that express CD40 on their surface, particularly by	
CC	introducing the nucleic acid molecule into the cells, and used to	
CC	treat conditions characterised by an aberrant or unwanted level of	
CC	CD40 mediated intracellular signalling, such as organ rejection, or	
CC	a CD40 dependent immune response in a subject receiving gene	
CC	therapy. The condition may be an allergic response or an	
CC	autoimmune response, or may be dependent on CD40 ligand-induced	
CC	activation of epithelial cells; an inflammatory kidney disease, a	
CC		

CC smooth muscle cell-dependent disease, or a condition associated
CC with Epstein-Barr virus.
SQ Sequence 665 AA;

Query Match 93.8%; Score 2820; DB 1; Length 665;
Best Local Similarity 95.1%; Pred. No. 4,9e-214;
Matches 540; Conservative 0; Mismatches 2; Indels 26; Gaps 2;

QY 1 MESSKMDSPGALQTNPKLHTDRSAGTPVPPGQKKEFKVTEDEKCEKCHLV 60
DB 123 MESSKMDSPGALQTNPKLHTDRSAGTPVPPGQKKEFKVTEDEKCEKCHLV 182
QY 61 CSPKQTECHRCESCMALLSSSPKTCACQESTYKDVFNQCKREILALQIYCRNE 120
DB 183 CSPKQTECHRCESCMALLSSSPKTCACQESTYKDVFNQCKREILALQIYCRNE 242
QY 121 SSGCAEQMLG-H-LVHLKNDCHFEELPCVRPDKCEKVKLRKLDHVEKACKYREATCSHC 179
DB 243 SSGCAEQMLG-H-LVHLKNDCHFEELPCVRPDKCEKVKLRKLDHVEKACKYREATCSHC 302
QY 180 KSOVPMIALQKHEDTDCPCVVVSCPHKCSVQTLNSELSAHLSECVNADSTCSFKRYGCV 239
DB 303 KSOVPMIALQKHEDTDCPCVVVSCPHKCSVQTLNSELSAHLSECVNADSTCSFKRYGCV 339
QY 240 FQGTNOQIAHBSASSAVQVHNLKEMNSLEKVSILLQNESVEKNSISLHNOICSEFI 299
DB 340 --GTNNOIAHBSASSAVQVHNLKEMNSLEKVSILLQNESVEKNSISLHNOICSEFI 397
QY 300 EIEROKEMLRNNEKSLHLQRYVIDSOAEKLEKELRPFQRMWEADSMKSSVESLQNR 359
DB 398 EIEROKEMLRNNEKSLHLQRYVIDSOAEKLEKELRPFQRMWEADSMKSSVESLQNR 457
QY 360 VTELESVDKSAQOVARNGLLSQSLSRHDQMLSVHDIRLADMDLGFQVLETAASYNGVLIM 419
DB 458 VTELESVDKSAQOVARNGLLSQSLSRHDQMLSVHDIRLADMDLGFQVLETAASYNGVLIM 517
QY 420 KIRDYRRKROEAVMGKTLISYQPFYTGFGYKMCARVYLNDGMRGTHLSLFEVIMRG 479
DB 518 KIRDYRRKROEAVMGKTLISYQPFYTGFGYKMCARVYLNDGMRGTHLSLFEVIMRG 577
QY 480 EYDALPMPFKOKVTLMLMDQSSRRHLGDARFDPNNSSEFKKPTGEMNIAAGCPVFAVQ 539
DB 578 EYDALPMPFKOKVTLMLMDQSSRRHLGDARFDPNNSSEFKKPTGEMNIAAGCPVFAVQ 637
QY 540 TVLENGTYIKDDTIFIKVIVDTSDDLDP 567
DB 638 TVLENGTYIKDDTIFIKVIVDTSDDLDP 665

RESULT 7
K98833
ID R98833 standard; Protein: 543 AA.
AC R98833;
DE CD40 associated protein (CAP)-1.
KW CD40 associated protein; CAP; agonist; antagonist; gene therapy;
OS cell proliferation; treatment; cancer; autoimmune disease.
OS Homo sapiens.
FH Key
FT Domain Location/Qualifiers
FT 53..91
FT /note="RING finger domain"
FT 117..141
FT /note="Zinc finger domain 1"
FT 148..170
FT /note="Zinc finger domain 2"
FT 177..197
FT /note="Zinc finger domain 3"
FT 384..540
FT /note="TRAF domain"
PN W09616665-A1.
PD 06-JUN-1996.
PF 04-DEC-1995; U15695.

PR 02-DEC-1994; US-349357.
PA (LJOL-) LA JOLIA CANCER RES FOUND.
PI Reed JC, Sato T;
DR WPT: 96-286818/29.
DR N-PSDB: T30773.
PT New CD40 associated protein, agonists and antagonists - used to
PI modulate cell proliferation, immune response, apoptosis etc., e.g.
PI for treating cancer or autoimmune disease
PS Claim 3, Fig 1: 94pp: English.
CC This is a CD40 associated protein (CAP)-1. This CAP is a protein that
CC specifically binds to CD40, a cell surface receptor involved in
CC apoptosis. Agonists and antagonists of CAP can increase or decrease
CC the level of CAP expression in a cell and can thereby modulate the
CC function of the cell. Such compounds can be used to treat cancer,
CC autoimmune diseases like asthma, hay fever, rheumatoid arthritis and
CC immunodeficiency diseases and neurodegeneration. Antibodies that bind
CC specifically to CAP can be used to assay CAP, to detect pathologically
CC altered levels. The encoding nucleic acid can be used to identify
CC related genes and to express CAP for gene therapy.
SQ Sequence 543 AA;

Query Match 93.3%; Score 2804; DB 1; Length 543;
Best Local Similarity 94.7%; Pred. No. 6.6e-213;
Matches 538; Conservative 0; Mismatches 4; Indels 26; Gaps 2;

QY 1 MESSKMDSPGALQTNPKLHTDRSAGTPVPPGQKKEFKVTEDEKCEKCHLV 60
DB 1 MESSKMDSPGALQTNPKLHTDRSAGTPVPPGQKKEFKVTEDEKCEKCHLV 60
QY 61 CSPKQTECHRCESCMALLSSSPKTCACQESTYKDVFNQCKREILALQIYCRNE 120
DB 61 CSPKQTECHRCESCMALLSSSPKTCACQESTYKDVFNQCKREILALQIYCRNE 120
QY 121 SSGCAEQMLG-H-LVHLKNDCHFEELPCVRPDKCEKVKLRKLDHVEKACKYREATCSHC 179
DB 121 SSGCAEQMLG-H-LVHLKNDCHFEELPCVRPDKCEKVKLRKLDHVEKACKYREATCSHC 180
QY 180 KSOVPMIALQKHEDTDCPCVVVSCPHKCSVQTLNSELSAHLSECVNADSTCSFKRYGCV 239
DB 181 KSOVPMIALQKHEDTDCPCVVVSCPHKCSVQTLNSELSAHLSECVNADSTCSFKRYGCV 217
QY 240 FQGTNOQIAHBSASSAVQVHNLKEMNSLEKVSILLQNESVEKNSISLHNOICSEFI 299
DB 218 --GTNNOIAHBSASSAVQVHNLKEMNSLEKVSILLQNESVEKNSISLHNOICSEFI 275
QY 300 EIEROKEMLRNNEKSLHLQRYVIDSOAEKLEKELRPFQRMWEADSMKSSVESLQNR 359
DB 276 EIEROKEMLRNNEKSLHLQRYVIDSOAEKLEKELRPFQRMWEADSMKSSVESLQNR 335
QY 360 VTELESVDKSAQOVARNGLLSQSLSRHDQMLSVHDIRLADMDLGFQVLETAASYNGVLIM 419
DB 336 VTELESVDKSAQOVARNGLLSQSLSRHDQMLSVHDIRLADMDLGFQVLETAASYNGVLIM 395
QY 420 KIRDYRRKROEAVMGKTLISYQPFYTGFGYKMCARVYLNDGMRGTHLSLFEVIMRG 479
DB 396 KIRDYRRKROEAVMGKTLISYQPFYTGFGYKMCARVYLNDGMRGTHLSLFEVIMRG 455
QY 480 EYDALPMPFKOKVTLMLMDQSSRRHLGDARFDPNNSSEFKKPTGEMNIAAGCPVFAVQ 539
DB 456 EYDALPMPFKOKVTLMLMDQSSRRHLGDARFDPNNSSEFKKPTGEMNIAAGCPVFAVQ 515
QY 540 TVLENGTYIKDDTIFIKVIVDTSDDLDP 567
DB 516 TVLENGTYIKDDTIFIKVIVDTSDDLDP 543

RESULT 8
W27436
ID W27436 standard; Protein: 516 AA.
AC W27436;
DE 27-MAR-1998 (first entry)
PF Human CRAFT-b isoform p70del8.9.

KM CD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human;
 KM CD40 mediated intracellular signalling; organ rejection; allergy;
 KM hay fever; autoimmune disease; systemic lupus erythematosus;
 KM rheumatoid arthritis; myasthenia gravis; Graves' disease;
 KM idiopathic thrombocytopenia purpura; haemolytic anaemia;
 KM diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
 KM apoptosis; Riecher's syndrome; spondyloarthritis; Lyme disease; HIV;
 KM syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
 KM pneumoconiosis; adult respiratory distress syndrome; pneumonitis;
 KM asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
 KM glomerulosclerosis; multiple sclerosis; glomerulonephritis;
 KM glomerulonephritis; leprosy; malaria; Goodpasture's disease;
 KM Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
 KM Wegener's granulomatosis; cryoglobulinemia;
 KM Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
 KM AIDS; oesophageal dysmotility; inflammatory bowel disease;
 KM Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
 KM gene therapy; diagnosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 52..122
 FT /label="CRAF-b domain
 FT /note="Claim 1"
 FT 239..263
 FT Region /note="zinc finger 1 (zn binding to Cys-239,
 FT Cys-246, His-258 and Cys-263)"
 FT 270..292
 FT Region /note="zinc finger 2 (zinc binding to Cys-270,
 FT Cys-275, His-287 and Cys-292)"
 FT Binding_site 16..19
 FT /note="putative SH3 binding motif"
 FT Binding_site 44..47
 FT /note="putative SH3 binding motif"
 FT Binding_site 103..110
 FT /note="putative SH3 binding motif"
 FT MO974473-A1.
 PD 25-SEP-1997. U05076.
 PE 21-MAR-1997. U05076.
 PR 18-SEP-1996; US-026584.
 PR 21-MAR-1996; US-013820.
 PR 01-MAY-1996; US-016626.
 PR 01-MAY-1996; US-016659.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PA Cleary AM, Frank DM, Lederman S;
 WP1: 97-479907/44.
 N-PSDB; T90123.
 PT Protein comprising CRAF1-b domain capable of inhibiting CD40
 PT mediated cell activation - useful to treat conditions characterised
 PT by aberrant or unwanted level of CD40 mediated intracellular
 PT signalling
 PT Example 1; Fig 1A-O; 158pp; English.
 CC This polypeptide comprises a CRAF1 (TRAF-3) protein designated
 CC p70del8.9 that is encoded by exons 1-2, 4-7 and 10-13 of the human
 CC CRAF gene (see T90123). Different isoforms (W27428-37) of CRAF1
 CC have been identified that arise from alternative splicing. CRAF1
 CC peptides comprising from 0-4 zinc finger domains, and nucleic acids
 CC encoding them, can be used to inhibit CD40 ligand activation of
 CC cells that express CD40 on their surface, particularly by
 CC introducing the nucleic acid molecule into the cells, and used to
 CC treat conditions characterised by an aberrant or unwanted level of
 CC CD40 mediated intracellular signalling, such as organ rejection, or
 CC a CD40 dependent immune response in a subject receiving gene
 CC therapy. The condition may be an allergic response or an
 CC autoimmune response, or may be dependent on CD40 ligand-induced
 CC activation of epithelial cells, an inflammatory kidney disease, a
 CC smooth muscle cell-dependent disease, or a condition associated
 CC with Epstein-Barr virus.
 CC Sequence 516 AA.

Best Local Similarity 90.3%; Pred. No. 5, 3e-201;
 Matches 513; Conservative 0; Mismatches 2; Indels 53; Gaps 2;
 QY 1 MESSKKNDSPGALQTNPLKHTDRSAGPVEPEOGYKEKFKVYEDKCKEKLTVL 60
 Db 1 MESSKKNDSPGALQTNPLKHTDRSAGPVEPEOGYKEKFKVYEDKCKEKLTVL 60
 QY 61 CSKQTECGHGFESCAALLSSSPKCTACQSYKDKYFKNDCKRETLAQYCRNE 120
 Db 61 CSKQTECGHGFESCAALLSSSPKCTACQSYKDKYFKNDCKRETLAQYCRNE 120
 QY 121 SRCAEOLMIGH-LVHLKNDCHFEELPCVPDPCKEKLRLDHDYKACKYREATCSHC 179
 Db 121 SRCAEOLMIGH-LVHLKNDCHFEELPCVPDPCKEKLRLDHDYKACKYREATCSHC 180
 QY 180 KSGVPMTALAKHEDTDCPCVVCSPHKCSVQTLRLSELNAHLECVNAPSTCSFKRYGCY 239
 Db 181 KSGVPMTALAKHEDTDCPCVVCSPHKCSVQTLRLSELNAHLECVNAPSTCSFKRYGCY 239
 QY 240 FQGTNOQIRKHEASSAVOHVNLKEMNSLEKRVSLQNSVEKNSISQSLHNOICFEI 299
 Db 190 -QGTNOQIRKHEASSAVOHVNLKEMNSLEKRVSLQNSVEKNSISQSLHNOICFEI 248
 QY 300 EIRROKEMLRNNEKTLHQRVIDSOAEKLEKDEIRPFROMWEADSKSSVESIQNR 359
 Db 249 EIRROKEMLRNNEKTLHQRVIDSOAEKLEKDEIRPFROMWEADSKSSVESIQNR 308
 QY 360 VTELESVDKASGAVARNTGLLESQLSRHQMLSVHDIRLADMQLGQVLETAASYGVLIW 419
 Db 309 VTELESVDKASGAVARNTGLLESQLSRHQMLSVHDIRLADMQLGQVLETAASYGVLIW 368
 QY 420 KIRDYRRKQEAVMGKTLSTISQPFYTGFGYKMCARVYINGMGMGKTLSTFVYIMRG 479
 Db 369 KIRDYRRKQEAVMGKTLSTISQPFYTGFGYKMCARVYINGMGMGKTLSTFVYIMRG 428
 QY 480 EYDALLPMPFKQVTLMLMDQSSRRHLGDAFPDPDPSSFFKPTGEMNTASGCPVFAO 539
 Db 429 EYDALLPMPFKQVTLMLMDQSSRRHLGDAFPDPDPSSFFKPTGEMNTASGCPVFAO 488
 QY 540 TVLENGTYIKDDTIFKVIYDTSDDLDP 567
 Db 489 TVLENGTYIKDDTIFKVIYDTSDDLDP 516
 RESULT 9
 W27437
 ID W27437 standard; Protein; 638 AA.
 AC W27437;
 DT 27-MAR-1998 (first entry)
 DE Human CRAF1-b isoform p70del8.9
 KM CD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human;
 KM CD40 mediated intracellular signalling; organ rejection; allergy;
 KM hay fever; autoimmune disease; systemic lupus erythematosus;
 KM rheumatoid arthritis; myasthenia gravis; Graves' disease;
 KM idiopathic thrombocytopenia purpura; haemolytic anaemia;
 KM diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
 KM apoptosis; Riecher's syndrome; spondyloarthritis; Lyme disease; HIV;
 KM syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
 KM pneumoconiosis; adult respiratory distress syndrome; pneumonitis;
 KM asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
 KM glomerulosclerosis; multiple sclerosis; glomerulonephritis;
 KM glomerulonephritis; leprosy; malaria; Goodpasture's disease;
 KM Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
 KM Wegener's granulomatosis; cryoglobulinemia;
 KM Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
 KM AIDS; oesophageal dysmotility; inflammatory bowel disease;
 KM Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
 KM gene therapy; diagnosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 52..122

Sat Sep 2 10:45:20 2000

us-09-224-556-2.1ag

FT /label= Craf-b-domain
FT /note= "Claim 1"
FT 239. .263
FT /note= "zinc finger 1 (zn binding to Cys-239,
FT Cys-246, His-258 and Cys-263)"
FT Region
FT 270. .292
FT /note= "zinc finger 2 (zinc binding to Cys-270,
FT Cys-275, His-287 and Cys-292)"
FT Binding_site
FT 16. .19
FT /note= "putative SH3 binding motif"
FT Binding_site
FT 44. .47
FT /note= "putative SH3 binding motif"
FT Binding_site
FT 103. .110
FT /note= "putative SH3 binding motif"
FT W09734473-A1.
FT 25-SEP-1997. 005076.
FT 21-MAR-1997. 005076.
FT 18-SEP-1996. US-026584.
FT 21-MAR-1996. US-013820.
FT 01-MAY-1996. US-016626.
FT 01-MAY-1996. US-016659.
FT (UYCO) UNIV COLUMBIA NEW YORK.
FT Cleary AM, Frank DM, Lederman S;
FT WPI: 97-479907/44.
DR N-PSDB: T90123.
DR Protein comprising Craf1-b domain capable of inhibiting CD40
PT mediated cell activation - useful to treat conditions characterised
PT by aberrant or unwanted level of CD40 mediated intracellular
PT signalling
PT Example 1: Fig 1A-O: 158bp; English.
PT This polypeptide comprises a Craf1 (TRAF-3) protein designated
PT p70e1b, that is encoded by exons 1-2, 4-7 and 10-13 of the human
PT Craf1 gene (see T90123). Different isoforms (W27428-37) of Craf1
PT have been identified that arise from alternative splicing. Craf1
PT peptides comprising from 0-4 zinc finger domains, and nucleic acids
PT encoding them, can be used to inhibit CD40 ligand activation or
PT cells that express CD40 on their surface, particularly by
PT introducing the nucleic acid molecule into the cells, and used to
PT treat conditions characterised by an aberrant or unwanted level of
PT CD40 mediated intracellular signalling, such as organ rejection, or
PT a CD40 dependent immune response in a subject receiving gene
PT therapy. The condition may be an allergic response or an
PT autoimmune response, or may be dependent on CD40 ligand-induced
PT activation of epithelial cells, an inflammatory kidney disease, a
PT smooth muscle cell-dependent disease, or a condition associated
PT with Epstein-Barr virus.
PT Sequence 638 AA;
SO
Query Match 88.3%; Score 2652.5; DB 1; Length 638;
Best Local Similarity 90.3%; Pred. No. 7.1e-201; Indels 53; Gaps 2;
Matches 513; Conservative 0; Mismatches 2;
OY 1 MESSKKMSPGALQTNPLKLTDRSAGTPVPEOGGKYEKVEKCEKCHLY 60
DB 123 MESSKKMSPGALQTNPLKLTDRSAGTPVPEOGGKYEKVEKCEKCHLY 182
OY 61 CSFKOTEGCHRCESCMALLSSSPKCTACQESTIVDKVKNCKCKREILALOYCRNE 120
DB 183 CSFKOTEGCHRCESCMALLSSSPKCTACQESTIVDKVKNCKCKREILALOYCRNE 242
OY 121 SRGCAEQLMGR-LVHLKNDCHFEELPCVRPCKEKLVDLHVEKAKYREATCSHC 179
DB 243 SRGCAEQLMGR-LVHLKNDCHFEELPCVRPCKEKLVDLHVEKAKYREATCSHC 302
OY 180 KSOVPMALOKKHEDTDCPCVYVSCPHKCSVOLLNSELSAHLSVCVNPSPCSEFRYGCV 239
DB 303 KSOVPMALOKKHEDTDCPCVYVSCPHKCSVOLLNSELSAHLSVCVNPSPCSEFRYGCV 311
OY 240 FQGTNOQIKAHASAVOHNVLKESNSLEKYSLLQNSVEKKNKSIOSLHNOICSEFI 299
DB 312 -QGTNOQIKAHASAVOHNVLKESNSLEKYSLLQNSVEKKNKSIOSLHNOICSEFI 370

OY 300 EIEROKEMLRNNEKILHIOVIDSQAEKLEKDEIRPFROMWEADSMKSSVESLONR 359
DB 371 EIEROKEMLRNNEKILHIOVIDSQAEKLEKDEIRPFROMWEADSMKSSVESLONR 430
OY 360 VTELESVDKSAQAVARNTGLLESQLSRHDOMLSVHDIRLADMDLGFQVLETASYNGVLIW 419
DB 431 VTELESVDKSAQAVARNTGLLESQLSRHDOMLSVHDIRLADMDLGFQVLETASYNGVLIW 490
OY 420 KIDYKRRKQEAAMGKTLISLVSQPFYTGFGYKMCARVYLNGDMGKSTLSLFEVIMRG 479
DB 491 KIDYKRRKQEAAMGKTLISLVSQPFYTGFGYKMCARVYLNGDMGKSTLSLFEVIMRG 550
OY 480 EYDALLPWPEKQVITLMDQSSRHGDAKPPDNSSFFKPGEMNIASGCPVVAQ 539
DB 551 EYDALLPWPEKQVITLMDQSSRHGDAKPPDNSSFFKPGEMNIASGCPVVAQ 610
OY 540 TVLENGITKDDTIFIKVIVDTSIDLPDP 567
DB 611 TVLENGITKDDTIFIKVIVDTSIDLPDP 638
RESULT 10
W27434
W27434 standard; Protein: 512 AA.
ID 27-MAR-1998 (first entry)
AC Human Craf1 isoform p55del9,10.
DE Human Craf1 isoform p55del9,10.
KW CD40 receptor associated factor 1; Craf1-a; TRAF-3; p55; human;
KW CD40 mediated intracellular signalling; organ rejection; allergy;
KW hay fever; autoimmune disease; systemic erythematosis;
KW rheumatoid arthritis; myasthenia gravis; Graves' disease;
KW idiopathic thrombocytopenia purpura; haemolytic anaemia;
KW diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
KW apoptosis; Richter's syndrome; spondyloarthritis; Lyme disease; HIV;
KW syphilis; tuberculosis; adult respiratory distress syndrome; pneumonitis;
KW pneumoconiosis; Farmer's lung; hepatitis; cirrhosis;
KW glomerulosclerosis; multiple sclerosis; kidney disease; nephropathy;
KW atherosclerosis; glomerulopathy; Goodpasture's disease;
KW endocarditis; leprosy; malaria; polypariteritis; multiple myeloma;
KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
KW Wegener's granulomatosis; cryoglobulinemia; amyloidosis; Sjogren's syndrome;
KW Waldenstrom's macroglobulinemia; amyloidosis; Slogren's syndrome;
KW AIDS; oesophageal dysmotility; inflammatory bowel disease;
KW bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
KW Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
KW gene therapy; diagnosis.
OS Homo sapiens.
FH Key
FT Region 148. .170
FT /note= "zinc finger 1 (zn binding to Cys-117,
FT Cys-124, His-136 and Cys-141)"
FT Region 148. .170
FT /note= "zinc finger 2 (zinc binding to Cys-148,
FT Cys-153, His-165 and Cys-170)"
FT Region 148. .170
FT /note= "zinc finger 3 (zn binding to Cys-177,
FT Cys-180, His-192 and Cys-197)"
FT W09734473-A1.
FT 25-SEP-1997. 005076.
FT 21-MAR-1997. 005076.
FT 18-SEP-1996. US-026584.
FT 21-MAR-1996. US-013820.
FT 01-MAY-1996. US-016626.
FT 01-MAY-1996. US-016659.
FT (UYCO) UNIV COLUMBIA NEW YORK.
FT Cleary AM, Frank DM, Lederman S;
FT WPI: 97-479907/44.
DR N-PSDB: T90123.
DR Protein comprising Craf1-b domain capable of inhibiting CD40
PT mediated cell activation - useful to treat conditions characterised
PT by aberrant or unwanted level of CD40 mediated intracellular
PT signalling

PS Example 1: Fig 1D-O: 158pp: English.
 CC This polypeptide comprises a CRAF1 (TRAF-3) isoform designated
 CC p5delta19,10. It is encoded by exons 4-8 and 11-13 of the human
 CC CRAF gene (see 190123) and arises by alternative splicing of the
 CC sequence for CRAF1-a (see W27431), a signalling protein that
 CC interacts with the cytoplasmic tail of B cell surface molecule CD40
 CC and which mediates a variety of T-dependent effects on B cell
 CC activation and differentiation. A higher mol.wt. CRAF1, designated
 CC CRAF1b (see W27428) has also been identified, as well as isoforms
 CC p5 (see W27429), p15 (see W27430) and variants of CRAF-1a and
 CC CRAF-b (see W27432-37) that comprise different combinations of 5
 CC zinc fingers. CRAF1 peptides, comprising from 0-4 zinc finger
 CC domains, and nucleic acids encoding them, can be used to inhibit
 CC CD40 ligand activation of cells that express CD40 on their surface,
 CC particularly by introducing a nucleic acid molecule into the cells,
 CC and used to treat conditions characterised by an aberrant or
 CC unwanted level of CD40 mediated intracellular signalling, such as
 CC organ rejection, or a CD40 dependent immune response in a subject
 CC receiving gene therapy. The condition may be an allergic response
 CC or an autoimmune response, or may be dependent on CD40 ligand-
 CC induced activation of epithelial cells, an inflammatory kidney
 CC disease, a smooth muscle cell-dependent disease, or a condition
 CC associated with Epstein-Barr virus.
 SQ Sequence 512 AA;

Query Match 88.1%; Score 2646.5; DB 1; Length 512;
 Best Local Similarity 89.6%; Pred. No. 1.6e-200;
 Matches 509; Conservative 0; Mismatches 2; Indels 57; Gaps 2;

OY 1 MESSKKMSPGALQTNPPKLTHTDSAGTPVPVPOGGYKKEFVTVKEKYCKECHLVL 60
 DB 1 MESSKKMSPGALQTNPPKLTHTDSAGTPVPVPOGGYKKEFVTVKEKYCKECHLVL 60
 OY 61 CSPKQTEGHRCESCMAALLSSSSPKCTACQESTYKDKVFKNCKREITLALQTYCRNE 120
 DB 61 CSPKQTEGHRCESCMAALLSSSSPKCTACQESTYKDKVFKNCKREITLALQTYCRNE 120
 OY 121 SRGCAEQMLGCH-LVHLKNDCHFEELPCVPRDCKEKVLRKDLRDHYEKACKYREATCSHC 179
 DB 121 SRGCAEQMLGCH-LVHLKNDCHFEELPCVPRDCKEKVLRKDLRDHYEKACKYREATCSHC 180
 OY 180 KSOVMILQKHEDTDCVYVSCPHKCSVOYLLRSELSAHLSECVNAPSTCSFRYRGV 239
 DB 180 KSOVMILQKHEDTDCVYVSCPHKCSVOYLLRSELSAHLSECVNAPSTCSFRYRGV 239
 OY 191 KSQVMILQKHEDTDCVYVSCPHKCSVOYLLRSELSAHLSECVNAPSTCSFRYRGV 239
 DB 191 KSQVMILQKHEDTDCVYVSCPHKCSVOYLLRSELSAHLSECVNAPSTCSFRYRGV 239
 OY 240 FQGTNQAIKAEASAVOHVNLKEMSNLSLEKVSILQNSVEYKKNKSIQSLNQCISFEI 299
 DB 240 FQGTNQAIKAEASAVOHVNLKEMSNLSLEKVSILQNSVEYKKNKSIQSLNQCISFEI 299
 OY 218 -----VSLQNSVEYKKNKSIQSLNQCISFEI 244
 DB 218 -----VSLQNSVEYKKNKSIQSLNQCISFEI 244
 OY 300 EIERQKEMLRNNESKILHLQRYVDSQAELKELDKKEIRPFQONWEADSMKSSVESLQNR 359
 DB 300 EIERQKEMLRNNESKILHLQRYVDSQAELKELDKKEIRPFQONWEADSMKSSVESLQNR 359
 OY 245 EIERQKEMLRNNESKILHLQRYVDSQAELKELDKKEIRPFQONWEADSMKSSVESLQNR 304
 DB 245 EIERQKEMLRNNESKILHLQRYVDSQAELKELDKKEIRPFQONWEADSMKSSVESLQNR 304
 OY 360 VTELESVNSKAGVARNGLLESQSLSRHQMLSVHDIRLADMDLGRFOVLETSYNGVLIW 419
 DB 360 VTELESVNSKAGVARNGLLESQSLSRHQMLSVHDIRLADMDLGRFOVLETSYNGVLIW 419
 OY 305 VTELESVNSKAGVARNGLLESQSLSRHQMLSVHDIRLADMDLGRFOVLETSYNGVLIW 364
 DB 305 VTELESVNSKAGVARNGLLESQSLSRHQMLSVHDIRLADMDLGRFOVLETSYNGVLIW 364
 OY 420 KIRQYKRRKQAEVAMGKTLISLYSQPYTGYFGYKMCARVYLNDGNGKGNHLSLFEYIMNG 479
 DB 420 KIRQYKRRKQAEVAMGKTLISLYSQPYTGYFGYKMCARVYLNDGNGKGNHLSLFEYIMNG 479
 OY 480 EYDALLPMPFKQKVTLMMDQSSRRHLGDAFKPDPNSSSFFKPTGEMNIASGCPVFAVQ 539
 DB 480 EYDALLPMPFKQKVTLMMDQSSRRHLGDAFKPDPNSSSFFKPTGEMNIASGCPVFAVQ 539
 OY 425 EYDALLPMPFKQKVTLMMDQSSRRHLGDAFKPDPNSSSFFKPTGEMNIASGCPVFAVQ 484
 DB 425 EYDALLPMPFKQKVTLMMDQSSRRHLGDAFKPDPNSSSFFKPTGEMNIASGCPVFAVQ 484
 OY 540 TVLENGTYKKDDTIFIKVIVDTSDLPDP 567
 DB 540 TVLENGTYKKDDTIFIKVIVDTSDLPDP 567
 OY 485 TVLENGTYKKDDTIFIKVIVDTSDLPDP 512
 DB 485 TVLENGTYKKDDTIFIKVIVDTSDLPDP 512

RESULT 11
 W27435

ID W27435 standard: Protein: 634 AA.
 AC W27435:
 DE 27-MAR-1998 (first entry)
 KW Human CRAF1-b isoform p70delta19,10.
 KW CD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human;
 KW CD40 mediated intracellular signalling; organ rejection; allergy;
 KW hay fever; autoimmune disease; systemic lupus erythematosus;
 KW rheumatoid arthritis; myasthenia gravis; Graves' disease;
 KW idiopathic thrombocytopenia purpura; haemolytic anaemia;
 KW diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
 KW apoptosis; Rietel's syndrome; spondyloarthritis; Lyme disease; HIV;
 KW syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
 KW pneumoconiosis; adult respiratory distress syndrome; pneumonitis;
 KW asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
 KW atherosclerosis; multiple sclerosis; glomerulonephritis;
 KW glomerulocystitis; glomerulopathy; kidney disease; nephropathy;
 KW endocarditis; leprosy; malaria; Goodpasture's disease;
 KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
 KW Wegener's granulomatosis; cryoglobulinemia;
 KW Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
 KW AIDS; oesophageal dysmotility; inflammatory bowel disease;
 KW bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
 KW Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
 KW gene therapy; diagnosis.
 OS Homo sapiens.
 FH Key
 FT Domain
 FT /label= "CRAF-b domain
 FT /note= "Claim 1"
 FT Region
 FT /note= "zinc finger 1 (2n binding to Cys-239,
 FT Cys-246, His-258 and Cys-263)"
 FT Region
 FT /note= "zinc finger 2 (zinc binding to Cys-270,
 FT Cys-275, His-287 and Cys-292 "
 FT Region
 FT /note= "zinc finger 3 (2n binding to Cys-299,
 FT Cys-302, His-314 and Cys-319"
 FT Binding_site
 FT /note= "putative SH3 binding motif"
 FT Binding_site
 FT /note= "putative SH3 binding motif"
 FT Binding_site
 FT /note= "putative SH3 binding motif"
 FT Binding_site
 FT /note= "putative SH3 binding motif"
 PN W09734473-A1.
 PD 25-SEP-1997.
 PF 21-MAR-1997; U05076.
 PR 18-SEP-1996; US-026584.
 PR 21-MAR-1996; US-013820.
 PR 01-MAY-1996; US-016826.
 PR 01-MAY-1996; US-016659.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PI Cleary AM, Frank DM, Lederman S;
 DR MPI: 97-479907/44.
 DR N-PSDB: 790123.
 DE Protein capable of inhibiting CD40
 DE mediated cell activation - useful to treat conditions characterised
 DE by aberrant or unwanted level of CD40 mediated intracellular
 DE signalling
 PS Example 1: Fig 1A-O: 158pp: English.
 CC This polypeptide comprises a CRAF1 (TRAF-3) protein designated
 CC p70delta19,10 that is encoded by exons 1-2, 4-8 and 11-13 of the human
 CC CRAF gene (see 190123). Different isoforms (W27428-37) of CRAF1
 CC have been identified that arise from alternative splicing. CRAF1
 CC peptides comprising from 0-4 zinc finger domains, and nucleic acids
 CC encoding them, can be used to inhibit CD40 ligand activation of
 CC cells that express CD40 on their surface, particularly by
 CC introducing the nucleic acid molecule into the cells, and used to
 CC treat conditions characterised by an aberrant or unwanted level of
 CC CD40 mediated intracellular signalling, such as organ rejection, or
 CC a CD40 dependent immune response in a subject receiving gene
 CC therapy. The condition may be an allergic response or an
 CC autoimmune response, or may be dependent on CD40 ligand-induced

CC activation of epithelial cells, an inflammatory kidney disease, a
 CC smooth muscle cell-dependent disease, or a condition associated
 CC with Epstein-Barr virus.
 SQ Sequence 634 AA:

Query Match 88.1%; Score 2646.5; DB 1; Length 634;
 Best Local Similarity 89.6%; Pred. No. 2.1e-200;
 Matches 509; Conservative 0; Mismatches 2; Indels 57; Gaps 2;

1 MESSKMDSPGALQTNPLKHTDRSAGTPVPEEGGKKEKVEKEDKRCCKCHLVL 60
 123 MESSKMDSPGALQTNPLKHTDRSAGTPVPEEGGKKEKVEKEDKRCCKCHLVL 182
 61 CSPKQTECHRCESCMALLSSSPKCTACQESIVKDYFVDNCKREITLQIYCRNE 120
 183 CSPKQTECHRCESCMALLSSSPKCTACQESIVKDYFVDNCKREITLQIYCRNE 242
 121 SFGCAEQLMLGH-LVHLKNDCHFEELPCVPDCKEYLRKDLRDHYEKACKYREATCSHC 179
 243 SFGCAEQLMLGH-LVHLKNDCHFEELPCVPDCKEYLRKDLRDHYEKACKYREATCSHC 302
 180 KSOVPMIALQKHEDIDPCVAVVSCPHKCSVQTLRLSELSEAHLSGCYNAPSTCSFKRYGCV 239
 303 KSOVPMIALQKHEDIDPCVAVVSCPHKCSVQTLRLSELSEAHLSGCYNAPSTCSFKRYGCV 339
 240 FQGTNOQIKAHASSAVOHVNLKEMNSLEKKVSLQNESVEKNSISQSLHNOICSEFI 299
 340 FQGTNOQIKAHASSAVOHVNLKEMNSLEKKVSLQNESVEKNSISQSLHNOICSEFI 366
 300 ETEROKEMLRNNSKTLHQRVIDSOAEKLEKELKEIRPROMWEADSKSSVESLQNR 359
 367 ETEROKEMLRNNSKTLHQRVIDSOAEKLEKELKEIRPROMWEADSKSSVESLQNR 426
 360 VTELESVDKAGVAVANTGLESQSLSRHOMLSVHDIRLADMDLGFQVLETSYNGVLIM 419
 427 VTELESVDKAGVAVANTGLESQSLSRHOMLSVHDIRLADMDLGFQVLETSYNGVLIM 486
 420 KIRDYRRRQEAVMGKTLISLYSOPFTYGYFKMCAKVYLNGDMGKGTLSLFEVIMNG 479
 487 KIRDYRRRQEAVMGKTLISLYSOPFTYGYFKMCAKVYLNGDMGKGTLSLFEVIMNG 546
 480 EYDALLPMPFKOKVTMLMDQSSRRHLGDAFKPDNNSSEFKPTGEMNIASGCPVFAVQ 539
 547 EYDALLPMPFKOKVTMLMDQSSRRHLGDAFKPDNNSSEFKPTGEMNIASGCPVFAVQ 606
 540 TVLENGTYIKDITFIKVIYDTSDDLP 567
 607 TVLENGTYIKDITFIKVIYDTSDDLP 634

RESULT 12
 ID R98835
 AC R98835:
 DT 23-MAR-1998 (first entry)
 DE CD40 associated protein (CAP)-1 clone psk-7 (residues 82-543).
 KW CD40 associated protein; CAP; agonist; antagonist; gene therapy;
 KW cell proliferation; treatment; cancer; autoimmune disease.
 OS Homo sapiens.
 PN WO961665-A1.
 PD 06-JUN-1996.
 PR 04-DEC-1995; U15695.
 PR 02-DEC-1994; U5-349357.
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 PI Reed JC, Sato T;
 DR WPI: 96-286818/29.
 PT New CD40 associated protein, agonists and antagonists - used to
 PT modulate cell proliferation, immune response, apoptosis etc., e.g.
 PT for treating cancer or autoimmune disease
 PS Claim 5; Page -: 94pp; English.
 CC This is a clone of the CD40 associated protein (CAP)-1. This clone
 CC psk-7 encodes amino acids 82 to 543 of CAP-1. The CAP specifically binds

CC to CD40, a cell surface receptor involved in apoptosis. Agonists and
 CC antagonists of CAP can increase or decrease the level of CAP expression
 CC in a cell and can thereby modulate the function of the cell. Such
 CC compounds can be used to treat cancer, autoimmune diseases like asthma,
 CC hay fever, rheumatoid arthritis and immunodeficiency diseases and
 CC neurodegeneration. Antibodies that bind specifically to CAP can be used
 CC to assay CAP, to detect pathologically altered levels. The CAP-1 encoding
 CC nucleic acid can be used to identify related genes and to express CAP
 CC for gene therapy.
 CC Note: This sequence does not appear in the specification. It has
 CC been created from the parent CAP-1 sequence provided in Fig 1.
 SQ Sequence 472 AA:

Query Match 80.4%; Score 2416; DB 1; Length 472;
 Best Local Similarity 94.2%; Pred. No. 2e-182;
 Matches 467; Conservative 0; Mismatches 3; Indels 26; Gaps 2;

73 CESCMAALLSSSPKCTACQESIVKDYFKDNCCKREITLQIYCRNRCGAEQLMLGH 132
 2 CESCMAALLSSSPKCTACQESIVKDYFKDNCCKREITLQIYCRNRCGAEQLMLGH 61
 133 -LVHLKNDCHFEELPCVPDCKEYLRKDLRDHYEKACKYREATCSHCQVPMIALQKH 191
 62 LTVHLKNDCHFEELPCVPDCKEYLRKDLRDHYEKACKYREATCSHCQVPMIALQKH 121
 192 EDTDPCVAVVSCPHKCSVQTLRLSELSEAHLSGCYNAPSTCSFKRYGCVFQGTNOQIKAE 251
 122 EDTDPCVAVVSCPHKCSVQTLRLSELSEAHLSGCYNAPSTCSFKRYGCVFQGTNOQIKAE 156
 252 ASSAVOHNLEKEMNSLEKKVSLQNESVEKNSISQSLHNOICSEFIEIEROKEMLRNN 311
 157 ASSAVOHNLEKEMNSLEKKVSLQNESVEKNSISQSLHNOICSEFIEIEROKEMLRNN 216
 312 ESKILHLQRVIDSOAEKLEKELKEIRPROMWEADSKSSVESLQNRVTELESVDKAG 371
 217 ESKILHLQRVIDSOAEKLEKELKEIRPROMWEADSKSSVESLQNRVTELESVDKAG 276
 372 QVARTNGLESQSLSRHOMLSVHDIRLADMDLGFQVLETSYNGVLIMKIRYKRRQEA 431
 277 QVARTNGLESQSLSRHOMLSVHDIRLADMDLGFQVLETSYNGVLIMKIRYKRRQEA 336
 432 VNGKTLISLYSOPFTYGYFKMCAKVYLNGDMGKGTLSLFEVIMNGEYDALLPMPFKO 491
 337 VNGKTLISLYSOPFTYGYFKMCAKVYLNGDMGKGTLSLFEVIMNGEYDALLPMPFKO 396
 492 KYTLMMDQSSRRHLGDAFKPDNNSSEFKPTGEMNIASGCPVFAVQVLENGTYIKDD 551
 397 KYTLMMDQSSRRHLGDAFKPDNNSSEFKPTGEMNIASGCPVFAVQVLENGTYIKDD 456
 552 TFIKVIYDTSDDLP 567
 457 TFIKVIYDTSDDLP 472

RESULT 13
 ID W29257
 AC W29257:
 DT 18-MAR-1998 (first entry)
 DE Murine TRAF5, a novel TNF receptor associated factor family protein.
 KW TRAF5; tumour necrosis factor receptor; TNF;
 KW TNF signal transducer system.
 OS Murine sp.
 PN WO9731110-A1.
 PD 28-AUG-1997.
 PR 24-FEB-1997; J00512.
 PR 22-FEB-1996; JP-034674.
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 PI Nakano H, Nakata M, Okumura K, Yagita H;
 DR WPI: 97-435162/40.
 DR N-PDB: T87039.
 PT Tumour necrosis factor receptor associated factor family protein,

PT TRAF5 -useful to study signal transduction in tumour necrosis
PT factor receptor family
PS Claim 3; Pages 41-44; 69pp; Japanese.
CC The present sequence represents a novel protein, designated TRAF5, which
CC is a member of the tumour necrosis factor (TNF) receptor associated
CC factor family. The TRAF5 protein has a coiled-coil domain, a leucine
CC zipper motif and binds to lymphotoxin beta receptor and to CD30, but not
CC to CD40 or TNF receptor 2. TRAF5 and its corresponding DNA are useful for
CC the investigation of the signal transducer system of the TNF receptor
CC family and the functions of TRAF transducers. They can also be used as
CC probes for research and diagnostic purposes, and investigation of the
CC specific applications of potential therapeutic agents.
SQ Sequence 558 AA;

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Query Match Summary          41.4%: Score 1244; DB 1. Length 558;
Best Local Similarity       41.3%: Pred. No. 5e-90;
Matches 241; Conservative 113; Mismatches 163; Indels 66; Gaps 11.

QY 22 HDRSAGTP-VEVPBPG-----YKEFFVKTEVDKRYKCEKHLYLCPKQTECGH 70
Db 3 HSEEOAAVPCAFIRONGNSISLDFEDPTEYQFEQLEGRYKCAFCHVLAHPHQGC 62
QY 71 RCEECMAALLS-SSSPKRTACQESTYVKRYKVRKDNCKREKIELALQTYCNBSGCAQLM 129
Db 63 RFGQCCISLRLELNSVPLCPYDKVETKPEVBERKDNCKREVLNLHYCKN-APGCARII 121
QY 130 LG----HLVHLKNDHFEEELPCVRPDCKEKVVLRKDLADHVEAKCAKREATGSCSKQVPM 185
Db 122 LGRFDHLQ-----CSFAVPCPNCSCRAMLRKDYKELHLSAYCRREKCLYCKKDIYV 177
QY 186 IALQKHEDTDCPVVYVSCPHKCSVQTLRLSELSAHLSECVNAPSTCSFKRYGCVFQGINQ 245
Db 178 TMLADHEENSCPAYPVSCPNCRC-VQIIPRAVAVNHLTVCPLEADQDCPFKHGQGVYGGKG 236
QY 246 QIKAHSSAVQHVVLKLEKMSNLSLEKVSLLQNESVEKKSQSLQSLNQCSPEIETEROK 305
Db 237 NLEHERAALADMLLVLEKNTQLEORISDLQSLSEKQSKTQQLAEYKKEFEKELQFT 296
QY 306 EILRN-----ESKILHQRVDSQAEKLELDEKIRPFRQNMEE 345
Db 297 QMEGNGEFLSNVQALTSITTDKSNMLEAQRHLQLQVNOQPSRL-----D 341
QY 346 ADSMKSVESLQNRVTELESVDKSAGQVARNLTGLESQLSRHDOMLSVDIRLADMDLGF 405
Db 342 LRLSLDAVDSVQKRIQTLEASD-----QRLVLLLEGESKDAHINIKHAQINKNEERF 394
QY 406 QVLEFASTNGVLIKTKIRDTKROEAVMGKTLISLSQPYTGTGYKKCARVYLVNDGKG 465
Db 395 KOLEGACYSGKLIWYTDYRVKRRKEAVEGHTSVSPQPYTSRCGTRLCARAYLVNDGSG 454
QY 466 KGTHTSLFPIVIRGVDALLPWFPRQKVTYLMMLDQSSSRHHGADAFKPPNSSFFKPPG 525
Db 455 KGTHTSLFPIVIRGVDALLPWFPRQKVTYLMMLDQSSSRHHGADAFKPPNSSFFKPPG 514
QY 536 EKNIASGCPVEVAQTVLN--GTYYKDDTIFIKVYIDTSDLPD 566
Db 515 EKNIASGCPREFVSHSTLENSKNTYIKDDTLFLKVAVDLDDLED 557

RESULT 14
ID W27609
AC W27609 standard; Protein; 558 AA.
DT 27-APR-1998 (first entry)
DE Murine TRAF5.
KW Murine; mouse; TRAF5; tumour necrosis factor; TNF; allergy;
KW receptor associated factor family; immunosation; treatment;
KW cell proliferation inhibitor; screening; inhibitor; regulator.
OS Mus sp.
PN W09738099-A1.
PD 16-OCT-1997.
PF 10-APR-1997; J01236.

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PR 25-DEC-1996; JP-355847.
PR 11-APR-1996; JP-113035.
PA (MOCH) MOCHIDA PHARM CO LTD.
PI Inoue J;
PI WPI: 97-512716/47.
DR N-PSDB: T88022.
DR TRAF5, protein of tumour necrosis factor receptor associated factor
PT family - useful in immunisation, to treat allergies and as cell
PT proliferation inhibitor
PS Claim 2: Pages 41-44; 80pp; Japanese.
CC The present sequence is murine TRAF5 a protein of the tumour
CC necrosis factor (TNF) receptor associated factor family. TRAF5
CC products can be used in immunisation, to treat allergies and as
CC cell proliferation inhibitors. They can also be used to screen for
CC TRAF5 inhibitors or regulators.
SQ Sequence 558 AA;

Query Match	Similarity	41.4%	Score 1244	DB 1	Length 558
Best Local Similarity	42.7%	Pred. No. 5e-90			
Matches	243	Conservative 115	Mismatches 173	Indels	Gaps
QY	22	HTDSAGTP-VFVPEQGG-----YKEFEVTVEDKCYCEKHVLVSPKQTEGCH	70		
DB	3	HSEEOAAPVCAFIARONSNSISLIDEPDPTLEYQFEOLEERGCACASHVAPNHQGC	62		
QY	71	RPCSCSMALLS-SSSPCTACQESIYVDKQVKNDCCKREILLALQYCNESRGCAEQLM	129		
DB	63	RFCQOCISLRELNSVPLICPVDKYEIKQDEYFKQDCCKREVLNHYLCAN-APGCARDI	121		
QY	130	IG----HIVHLKNDCHFELPCVPDPCKEKLVRKDLRDHVEKAKYCREATCSHKQVPM	185		
DB	122	IGRFQDHLQH-----CSFQAVPCPNCSGRAMKRNQYKEHLSAYCPRFREKCLXCRDIYV	177		
QY	186	IALQKHEDTPCPCVYVSCPHKCSVOTLLRSELSAHLSBCVNAVSTQSEFKRYCCVFOGTNO	245		
DB	178	TNLQDHENSQPAVEVSPCPNRC-VOTIPRARVNEHLIYVCPAEODCCPFKHGCTVYGRKG	236		
QY	246	QIKAHASAVQHVVLTKEMSNLSKQVSLQNESVEKKKSIQSLHNOICSPREIEERCK	305		
DB	237	NLIEFERALADHMLLVLEKNTQLQKRSIDLQSLQSEQKSKIQQLALQYKATEKELEKQPT	296		
QY	306	EMLRNNSKILTHQAVIDISOAEKLELDEKLEIRPQK-NWE----EADSMKSSVESIQMR	359		
DB	297	QMGFGNGFFLSVQ-ALNSHTDKSAMLEQVQKQLQIYNQGSRRDLRSLVYAVDVSKR	355		
QY	360	VTELESVDKSAQVARNLTGLESQLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIM	419		
DB	356	ITQLFASD-----QRLVLEGGTSKHDHAINIKHAQNLNEBRPKOLEGACYSGLTIM	408		
QY	420	KIRDKRRKROEAVMKTISLYSQPPTYTGFGYKMCARUYLINDDGKSGKHTLSLFYIMNG	479		
DB	409	KATDVRKKREAVBEHTYVSFQSPPTYSCRGYLCARALINDGSGKGHLSLYEYVMQK	468		
QY	480	EYDALLPPKQVITLMLDQGSRRHLDGADKAPDPNSSSEFKKPTGEMNIASGCPFYVAQ	539		
DB	469	EBDSLLQMPFRQRYTLMLLDQSGKKNHLYETFKADPNSSSEFKRPGEMNIASGCPREYVH	528		
QY	540	TYLEN--GTIYKDTITFIKVIYVTSDDLQ	566		
DB	529	STLENSKNTYIKDPTLFLKVAVDLTDLED	557		
RESULT 15					
ID	W29258				
AC	W29258 standard; Protein: 557 AA.				
DT	18-MAR-1998 (first entry)				
DE	Human TRAF5, a novel TNF receptor associated factor family protein.				
KW	TRAF5, tumour necrosis factor receptor, TNF,				
OS	TNF signal transducer system.				
PN	Homo sapiens.				
PN	W0973110-A1				

PD 28-AUG-1997. J00512.
PR 24-FEB-1997. J00512.
PR 22-FEB-1996. JP-034674.
PA (SUME) SUMITOMO ELECTRIC IND CO.
PI Nakano H, Nakata M, Okumura K, Yagita H;
MPI: 97-435162/40.
DR N-PSDB: T87040.
DR Tumour necrosis factor receptor associated factor family protein,
PT TRAF5. Useful to study signal transduction in tumour necrosis
factor receptor family.
PS Claim 3: Pages 46-49, 69pp. Japanese.
CC The present sequence represents a novel protein, designated TRAF5, which
is a member of the tumour necrosis factor (TNF) receptor associated
factor family. The TRAF5 protein has a coiled-coil domain, a leucine
zipper motif and binds to lymphotoxin beta receptor and to CD30, but not
to CD40 or TNF receptor 2. TRAF5 and its corresponding DNA are useful for
the investigation of the signal transducer system of the TNF receptor
family and the functions of TRAF proteins. They can also be used as
probes for research and diagnostic purposes, and investigation of the
specific applications of potential therapeutic agents.

SO Sequence 557 AA;
Query Match 39.3%; Score 1182; DB 1; Length 557;
Best Local Similarity 41.6%; Pred. No. 3.8e-85;
Matches 229; Conservative 121; Mismatches 181; Indels 20; Gaps 8;
QY 25 RSAGTPEVPEQGGYKKEKYVEDKYCEKCHLVLCSPKOTEGHRCFSCMAALLS-S 83
DB 17 QNSGNSISIDFEPSIEFOYFERLEERKCAFCASHNPHQTCGHRFCOHCILSREIN 76
QY 84 SSPKCTAOESIVADKYFNKDCRREILALQIYCRNESGCAEOLMLGHLVHLKNDCHRE 143
DB 77 TVPICVDKEVIKSOEYFKDKCKREVILNYVCSN-APGCNAKVIILGRYODHLQOCLPQ 135
QY 144 ELPCVPRDCKEYKLDIDHVEKAKYREATCSHCQVPMIALOKHEPTDCPCVYVSC 203
DB 136 PVQCSNEKCRREVLRKDLKELHLSASCOFRKCKLYCKKDVVYVIMLNHEENLCPEYVFC 195
QY 204 PHKCSVOTLLRESELSEAHLSGCYNAFSTCSFRRYGCVEGTNOQIKAHBASAVOHNLLK 263
DB 196 PNNCA-KIILKEVEHHLAVCEPAEQDQPFHYGCAVTDKRRNLQOEHSHALREHMLVL 254
QY 264 EMSNSLEKRVSLQNESVEKNSIOSLNOJCSPEIEEROKEMLRNNESKILHLQVID 323
DB 255 EKNVQLEEQISDLHKSLEQKESKIOQLAETIKLEKEKOPAQLEFGKNGSLPNIQ-VFA 313
QY 324 SQAERKLEKDELRPF-----RONWEEADSKSSVESLQNRVTELESVDKSAGQVANT 377
DB 314 SHIDKSAMLEAOVHQLQAVNOQOKFDRPLMEAVDVKOKITLLENND-----QRL 366
QY 378 GILESOLSRHDOMLVHDIRLADMIDIGFOVLETASYNGVLYIKIRYKRRKOEAVMGKT 437
DB 367 AVLEEFENKHDTHINIHKAQLSKNERFKLIGTCTNGKILMKVTDYKKRKAENDGHTV 426
QY 438 SLXSQPFYGYGKMKCARVYLNGDMGKTHLSLFVYIMRGEYDALLPMPKQKVTML 497
DB 427 SIFSQSYTSCRGKLCARAYLNGDSGSHLSLYFVVRGGEFDSLQMPFRQRTML 486
QY 498 MDQSSRRHLGDAFKPDPNSSSKKPTGEMNIASGCPVFAQTVLEN--GYIKDDTIFI 555
DB 487 LDO-SGKKNIEMETFKPDPNSSSKKPDGEMNIASGCPVFAHSAVLNANAYIKDDTIFL 545
QY 556 KVIYVDTSDLPD 566
DB 546 KVAVDLTDLDD 556